

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Apr 20 15:17:56 2000; MasPar time 5.15 Seconds 600.911 Million cell updates/sec

Tabular output not generated.

Title:

Description: Perfect Score: Sequence: >US-09-150-947-12 (1-239) from USO9150947.pep 1763 1 ESQPDPKPDELHKSSKFTGL.....NKMYDSKDVKIEVYLTTKKK 239

Scoring table: PAM 150 Gap 11

Searched: 131253 seqs, 12956647 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-issued 1:5A\_COMB 2:5B\_COMB 3:PCT9\_COMB 4:backfiles1

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 30.280; Variance 145.353; scale 0.208

#### SUMMARIES

																							Result No.
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Sequence 12,	5	Sequence 5,	Sequence 24,	Sequence 22,	Sequence 7,	7,	ω `	w '	2	'n	Sequence 2,	1,	Sequence 11,	Sequence 11,	Sequence 10,	Sequence 10,	9	٥	4	•	Sequence 2,	Sequence 2,	Description
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45	44	43	42	41	40	39	38	37	36	ω 5	34	ω ω	32	31	30	29	28	27	26	25	
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## ALIGNMENTS

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TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE 255 AA; 30159 MW; 364503 CN;	3: 255	INFORMATION FOR SEO ID NO: 2:	TELEFAX: (303) 863-0223	TELECOMMUNICATION INFORMATION:	I NUMBE	REGISTRATION NUMBER: 33,005	Kowarik Togonh	CLASSIFICATION: 552	3-MAY	APPLICATION NUMBER: US/08/446,918A	SUFTWARE: PATENTIN RELEASE #1.U, Version #1.25 CURRENT APPLICATION DATA:	SYSTEM: PC-DOS/MS-DOS	₽	TYPE: F	COMPUTER READABLE FORM:	=	STATE: Colorado	Denver	Stree		SS	R OF SEQUENCES: 12	NVENTION: GENE T	APPLICANT: Elmslie, Robyn E.	2+0170	CHARDAY THOUSANDON.		•	Sequence 2, Application US/08446918A			200000		LT 1 US-08-446-918A-2 STANDARD; PRT; 255 AA.

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                                                                                                      TELEFAX: (303) 863-02
INFORMATION FOR SEQ ID NO:
                                                                                                                                           CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,0
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS
SOFTWARE: PatentIn Release (
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Dow, Steve W.
APPLICANT: Elmslie, Robyn E.
APPLICANT: Potter, Terence A.
APPLICANT: POTTER, TERENCE A.
TITLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL REGULATION
                                      MOLECULE TYPE:
ENCE 255 AA;
                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                          SEQUENCE CHARACTERISTICS:
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                                                                       LENGTH:
TYPE: 8
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                                                                                                     (303) 863-9700
(303) 863-0223
R SEQ ID NO: 2:
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30159 MW;
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Pred. No. 1.55e-143;
         Score 1760; DB 2;
Pred. No. 1.55e-143;
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                                                                              SEQUENCE
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GENERAL INFORMATION:
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                     11 DLRKKSELOGTALGNIKQIYYYNEKAKTENKESHDQFLQHTILFKGFFTDHSWYNDLLVD
                                                                                                                          TELEFAX: (303) 863-022 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                           CLASSIFICATION: 552
ATTORNEY/AGENT INFORMATION:
NAME: KOVARIK, JOSEPH E.
                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (303) 863-9700
                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                              MOLECULE TYPE: protein ENCE 233 AA; 27137 MW;
                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: GENE THERAPY FOR T CELL REGULATION
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                                                                                               TYPE: ami
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                                                                                                                                                                                                                         FILING DATE: 18-MAY-1995
                                                                                                                                                                                                                                                                                                           COUNTRY:
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1700 Lincoln Street, Suite 3500
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                                                 Score 375; DB 1;
Pred. No. 9.01e-22;
                                        56; Mismatches
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121 EEKKVPINLWLDGKQNTVPLETVKTNKKNVTVQELDLQARRYLQEKYNLYNSDVFDGKVQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: DOW, Steve W.
APPLICANT: Elmslie, Robyn E.
APPLICANT: Potter, Terence A.
TITLE OF INVENTION: GENE THEF
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                                                                                            Local Similarity
nes 82; Conser
                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:

NAME: Connell, Gary J.

REGISTRATION NUMBER: 32,020

REFERENCE/DOCKET NUMBER: 2879

TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
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                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 233 AA; 27137 MW;
                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                    FDSKDIVDKYKGKKVDLYGAYYGYQC-----AGG--T--PNK-TACMYGGVTLHDNNRLT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EEKKVPINLWLDGKQNTVPLETVKTNKKNVTVQELDLQARRYLQEKYNLYNSDVFDGKVQ 180
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                                                      ELHKSSKFTGL-MENMK-VLYDDNHVSAINVKSIDQFLYFDLIYSIKDTKLGNYDNVRVE 67
                                                                                                                                                                                                                                                                                                                                                 ZIP:
                                                                                                                                                                                                                                                             CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                CITY: Denver
STATE: Colorado
                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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larity 35.0%;
Conservative
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(303) 863-0223
R SEQ ID NO: 4:
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Pred. No. 9.01e-22;
56; Mismatches 77;
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                                                                                                                                                                                                                                                                                                                                                                                   Suite 3500
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                                                                                                            Length 233;
                                                                                           Indels 19;
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                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9, Application US/08876781 Patent No. 5872233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No.
                                                                                                                                                                                                                                                                                                                                          TELEFAX: (801)566-075 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: M. Wayne Western
REGISTRATION NUMBER: 22,788
REFERENCE/DOCKET NUMBER: T676
TELECOMMUNICATION INFORMATION:
TELEPHONE: (801)566-6633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Diskette, 3.5 inch, COMPUTER: AST Advantage NB-SX20 OPERATING SYSTEM: DOS 5.00 SOFTWARE: Word Perfect 5.1 CURRENT APPLICATION DATA:
                IDENTIFICATION METHOD: IDENTIFICATION METHOD: PUBLICATION INFORMATION:
                                                                                                                                                                                                             MOLECULE TYPE: peptide FRAGMENT TYPE: interna ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 84070
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Thorpe, N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Cole, Barry C.
APPLICANT: Atkin, Curtis L.
APPLICANT: Pole, Ann
APPLICANT: Oliphant, Arnold
                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Mycopla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KYRSITVRVFEDGK-NLLSFD-VQTNKKKVTAQELDYLTRHYLVKNKKLYEFN--NSPYE
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                                                                                                       NAME/KEY:
                                                                                                                                                             STRAIN: S
                                                                                                                                                                                                                                                                   TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                             ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/876,781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
 AUTHORS:
                                                                      LOCATION:
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                                                                                                                                                                                                                                                                                                                                                          (801)566-0750
Jones, C.L.
                                                                                                                                                                                             Staphylococcus aureus
                                                                      residues 39
                                                                                                    staphylococcal enterotoxin B amino acid sequence having sequence similarity to
                                                                                         sequence having MAM.
                                                                                                                                                             unicellular organism
                                                                                                                                                                                                                                  internal fragment
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                                                                      to 65
                                                                                                                                                                                                                                                                                                                                            9..
                                   sequence similarities.
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ORGANISM:

Staphylococcus aureus

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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS: Khan
TITLE: Nucleo
Patent No. 5872233
TITLE: Gene f.
                                                                                                                                                                                                                                                                                                                                                                                                         US-08-165-038-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                           Sequence 9, Application US/08165038
                                                                                                                                                                                                                                                                                                                                     Sequence 9, Application US/08165038 Patent No. 5639869
                                                                                                                                                                ZIP: 84070
COMPUTER READABLE FORM:
COMPUTER EADABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 72
COMPUTER: AST Advantage NB-SX20
COMPUTER: AST Advantage NB-SX20
OPERATING SYSTEM: DOS 5.00
SOFTWARE: World Perfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Cole, I
APPLICANT: Atkin,
                                                                                                                                                                                                                                                                                                                                                                                                                                       y Match 11.4%;
Local Similarity 100.0%;
nes 27; Conservative
                                                                    ATTORNEY/AGENT INFORMATION:
NAME: M. Wayne Western
REGISTRATION NUMBER: 22,788
REFERENCE/DOCKET NUMBER: T676
TELECOMMUNICATION INFORMATION:
TELEPHONE: (801)566-6633
                                     TELEFAX: (801)566-0750
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Thorpe, No. 5639869th &
STREET: 9035 South 700 East, Suite
                                                                                                                                                                                                                                                                    APPLICANT: Pole, Ann APPLICANT: Oliphant, Arnold TITLE OF INVENTION: Mycoplasma Arthritidis T-Cell TITLE OF INVENTION: Mitogen NUMBER OF SEQUENCES: 26
                                                                                                                    CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
 ORIGINAL SOURCE:
         MOLECULE TYPE:
FRAGMENT TYPE:
                                                                                                                                                                                                                               ADDANCE STREET: Sandy
                       TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                  APPLICATION NUMBER: US/08/165,038 FILING DATE:
                                                                                                                                                                                                                      COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ISSUE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL: J. VOLUME: 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : APR-1986
27 AA; 3270 MW; 3891 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene from Staphylococcus aureus
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                                                                                                                                                                                                                                                                                                    Cole, Barry C.
Atkin, Curtis L.
Pole, Ann
                                                    : (801)566-0750
(801)566-0750
---- Th NO: 9:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Khan, S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Bacteriol
        internal fragment
              peptide
                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 201; DB 2;
Pred. No. 1.93e-07;
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RESULT
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Best Local Similarity 100.0%;
Matches 27; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE: Nucleo Patent No. 5639869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. 5872233
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10, Application US/08876781
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IDENTIFICATION METHOD:
PUBLICATION INFORMATION:
AUTHORS: Jones, C.L.
AUTHORS: Khan, S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KSIDQFLYFDLIYSIKDTKLGNYDNVR 27
                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch,
COMPUTER: AST Advantage NB-SX20
OPERATING SYSTEM: DOS 5.00
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: M. Wayne Western
REGISTRATION NUMBER: 22,
                                                               CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Thorpe, No.
STREET: 9035 South 700
                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Mycopla-
TITLE OF INVENTION: Mitogen
NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Atkin, Cui
APPLICANT: Pole, Ann
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Oliphant, Arnold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                    STREET: 9035
CITY: Sandy
STATE: Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL:
VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
NAME/KEY:
LOCATION:
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DATE: APR-1986
NCE 27 AA; 3270 MW; 3891 CN;
                                                   FILING DATE:
                                                                                                                     FILING DATE:
                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 84070
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleotide Sequence of the Enterotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cole, Barry C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Bacteriol.
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                                                                                                                                     US/08/876,781
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Pred. No. 1.93e-07;
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                                                                                                                                                                                                                    720 Kb storage
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Best Local
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                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                 Sequence 10, Application US/08165038
                                                                                                                                                                                                 XXXXXX
                                                                                                                                                                                                                                                                                                                                                                TITLE: Nucleotide Sequence of the Enterotoxin Patent No. 5872233
                                                                                                                                 Patent No. 5639869
GENERAL INFORMATION:
                                                                                                                                                  Sequence 10,
                                                                                                                                                                                                                                                                                                                  JOURNAL: J. Bacteriol.

VOLUME: 166
ISSUE: 1
PAGES: 29-33
DATF:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (801)566-0750
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
                                                                                                                                                                                                                                                                                                                                                                              IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
PUBLICATION INFORMATION:
AUTHORS: Jones, C.L.
AUTHORS: Khan, S.A.
                                                                                                                                                                                                                                                      1 TKLGNYDNYRVEFKNKDLADKYKDKYV 27
                                                                                 APPLICANT: Cole, Barry C.
APPLICANT: Atkin, Curtis L.
APPLICANT: Pole, Ann
APPLICANT: Oliphant, Arnold
TITLE OF INVENTION: Mycoplasma Arthritidis T-Cell
TITLE OF INVENTION: Micogen
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch,
COMPUTER: AST Advantage NB-SX20
                                                              ADDRESSEE: Thorpe, N
                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide FRAGMENT TYPE: internal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (801)566-6633
                            STREET: 9035
CITY: Sandy
STATE: Utah
COUNTRY: USA
                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                              TKLGNYDNVRVEFKNKDLADKYKDKYV
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                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CELL TYPE: unicellular organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN: S6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                          ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                            h 11.1%;
Similarity 100.0%;
27; Conservative
                                                                                                                                                                                                                                                                                                            : APR-1986
27 AA; 3265 MW;
                        84070
                                                                                                                                           J, Application US/08165038
5639869
                                                      E: Thorpe,
9035 South
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (801)566-0750
                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                             staphylococcal enterotoxin B amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                      residues 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence having sequence similarity
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                                                     No. 5639869th & Western
700 East, Suite 200
                                                                              26
                                                                                                                                                                                                                                                                                                            4119 CN;
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Pred. No. 4.81e-07;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                      computer searching for sequence similarities.
                                                                                                                                                                                                                                              82
                                                                                                                                                                                                               PRT;
        720
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        Kb storage
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                                                                                                                   US-08-165-038-11
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                                                                     Sequence 11, Application US/08165038
                                                                                                                                                                                                                                                                   TITLE: Nucleo
                                             Sequence 11, Application US/08165038 Patent No. 5639869
     GENERAL INFORMATION:
APPLICANT: Cole, Barry C.
APPLICANT: Atkin, Curtis L.
APPLICANT: Pole, Ann
APPLICANT: Oliphant, Arnold
                                                                                                                                                 56
                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                        FEATURE:
TITLE OF INVENTION: Mycoplasma Arthritidis T-Cell
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                                                                                                                                                                                                                            JOURNAL:
VOLUME:
ISSUE: 1
PAGES: 2
                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                     DATE:
                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                CELL TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                             TITLE:
                                                                                                                                                                                                                                                                                                                                                                              ORGANISM:
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Query Match 11.1%;
Best Local Similarity 100.0%;
Matches 27; Conservative
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                         IDENTIFICATION METHOD: compu
IDENTIFICATION METHOD: seque
PUBLICATION INFORMATION:
AUTHORS: Jones, C.L.
AUTHORS: Khan, S.A.
TITLE: Nucleotide Sequence o
                                                                             1 TKLGNYDNVRVEFKNKDLADKYKDKYV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER

APPLICATION NUMBER

FILTER
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TELECOMMUNICATION INFORMATION:
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LENGTH: 27 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION: NAME: M. Wayne Western
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                                                             TKLGNYDNVRVEFKNKDLADKYKDKYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: M. Wayne Western REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/165,038
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                                                                                                                                                                                                                                                                                          Gene from Staphylococcus aureus
                                                                                                                                                                                             AA; 3265 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (801)566-6633
(801)566-0750
                                                                                                                                                                                                                                                                                                                                                                                                                             residues 56 to 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           staphylococcal enterotoxin B amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence having sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unicellular organism
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          internal fragment
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STANDARD;
                                                                                                                                                                                             4119
                                                                                                                             Pred.
                                                                                                                                         Score 196; DB 1;
Pred. No. 4.81e-07;
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                                                                                                                                                                                                                                                                                                                                                                                             sequence similarities
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PRT;
27
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Sequence 11, Application US/08876781

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RESULT
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Best Local Similarity 61.5%;
Matches 16; Conservative
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REGISTRATION NUMBER: 22,788
REFERENCE/DOCKET NUMBER: T676
TELECOMMUNICATION INFORMATION:
TELEPAN: (801)566-653
TELEFAX: (801)566-0750
INFORMATION FOR SEQ ID NO: 11:
XXXXXX
                                 US-08-876-781-11
                                                                                                                                                                                                                                       SEQUENCE
                                                                                                   30
                                                                                                VOLUME: 200
VOLUME: 200
PAGES: 15-20
PATE: 1987
PATE: 1987
                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: residues 30 to 56 IDENTIFICATION METHOD: compu IDENTIFICATION METHOD: seque PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CELL TYPE: unicellular organism
FEATURE:
NAME/KEY: staphylococcal enterotoxin C1 amino acid
NAME/KEY: sequence having sequence similarity to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: DOS
SOFTWARE: WORD PERFECT
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
FRAGMENT TYPE: internal fragment
ORIGINAL SOURCE:
ORGANISM: Staphylococcus aureu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                 JOURNAL: MUL
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CITY: Sandy
STATE: Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
TYPE: a
                                                                                                                                                                                                                                                                                                                  AUTHORS: Bohach, G.A.
AUTHORS: Schlievert, P.M.
TITLE: Nucleotide sequence of the staphylococcal
TITLE: enterotoxin Cl gene and relatedness to
TITLE: other pyrogenic exotoxins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/165,038 FILING DATE:
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9035 South 700 East,
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AST Advantage NB-SX20
SYSTEM: DOS 5.00
Word Perfect 5.1
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                                 STANDARD;
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Pred. No. 1.52e+00;
4; Mismatches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                        sequence
                                                                                                                                                                                                                                                                                                                                                                                                                        computer searching for sequence similarities.
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                                 PRT;
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Matches
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INFORMATION FOR SEQ ID NO: 1)
SEQUENCE CHARACTERISTICS:
FRIGTH: 27 amino acids
                                         SEQUENCE
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         Local Similarity
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MEDIUM TYPE: Diskette
COMPUTER: AST Advanta
OPERATING SYSTEM: DOS
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FRAGMENT TYPE: 1
ORIGINAL SOURCE:
ORGANISM: Stap
                                                                                                                                   IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
PUBLICATION INFORMATION:
AUTHORS: Bohach, G.A.
                                                                                                                                                                                                                    CELL TYPE: unicellular organism FEATURE:
                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: T6
TELECOMMUNICATION INFORMATION:
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NAME: M. Wayne Western
REGISTRATION NUMBER: 22,
                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Word Perfect 5.1 CURRENT APPLICATION DATA:
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APPLICANT: Atkin, Cur
APPLICANT: Pole, Ann
APPLICANT: Oliphant,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                     AUTHORS: Schlievert, P.M.
TITLE: Nucleotide sequence of the staphylococcal
TITLE: enterotoxin Cl gene and relatedness to
TITLE: other pyrogenic exotoxins
JOURNAL: Mol. Gen. Genet.
                                                                                                                                                                                     NAME/KEY:
NAME/KEY:
NAME/KEY:
                                                                                                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE:
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CITY: Sandy
                                                    PAGES: 15-20
DATE: 1987
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                                                                                                                                                                              LOCATION:
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  16;
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                                        27 AA; 3107 MW; 4022 CN;
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 6.2%;
llarity 61.5%;
Conservative
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9035 South 700 East,
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Atkin, Curtis L.
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SYSTEM: DOS 5.00
Word Perfort
                                                                                                                                                                             residues 30 to 56
                                                                                                                                                                                      sequence having sequence similarity MAM.
                                                                                                                                                                                                                                         Staphylococcus aureus
                                                                                                                                                                                                           staphylococcal enterotoxin Cl amino acid
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                                                                                                                                                                                                                                                              internal fragment
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           Score 110; DB 2;
Pred. No. 1.52e+00;
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  Mismatches
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  6; Indels
                    Length 27;
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Best Local Similarity 28.9%;
Matches 24; Conservative
  US-08-261-825-2
                                                                                                                                                                            SEQUENCE
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                                            185 GYIK-FIENENSFWYDMMPAPGD 206
                                                                                   126 LDKYRSITVRVFEDGKN-LLSFDVQTNKKKVTAQELDYLTRHYLVKNKKLYEFNNSPYET 184
                                                                                                          192 LQLIRAI-LKVPEDPTQCFLLFANQTEKDIILREDLEELQARYPNRFKLWFTLDHPPKDW 250
                                                                251 AYSKGEVTADM-IR-EHLPAPGD 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30 DNHVSAINVKSIDQFLYFDLIYSIKD
                                                                                                                                                                                                           TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: line:
                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                       IMMEDIATE SOURCE:
LIBRARY: PROSNOT16
CLONE: 1709102
                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/94 FILING DATE: Filed Herewith PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                           TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS: ADDRESSEE: Incyte Pharmaceuticals,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Corley, Neil C.
TITLE OF INVENTION: ELECTRON TRANSPORT PROTEINS
                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                TELEFAX: 650-845-4166
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                                                                                                                                                                            305 AA; 34095 MW; 500339 CN;
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  STANDARD;
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                                                                                                                               Score 109; DB 2;
Pred. No. 1.78e+00;
25; Mismatches 29
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 PRT;
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 174 AA
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Matches 2
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                               Sequence
                                                                            XXXXX
                                                                                                 PCT-US95-07748A-2
Sequence 2, Application PC/TUS9507748A GENERAL INFORMATION:
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                                                                                                                                                              124 DYLIQLDSDKIDYAEKYGEKARENFEESY 152
                                                                                                                                                                                                                              / Match 5.6%;
Local Similarity 29.2%;
nes 26; Conservative
                                                                                                                                                                                                                                                                                                                                         TELEFAX: (619) 455-51 INFORMATION FOR SEQ ID NO:
                                                                                                                                           62 DN-VRVEFKNKDLADKYKDKYVDVFGANY
                                                                                                                                                                                                          65 AKAPEIRGSLRKIGIKEN-SVLLDALDVVGFIKSKITTDFLSFIIMNINSLIKGYPNSIF 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                    6 PKPDELHKSSKFTGLMENMKVLYDD-NHVSAINVKSIDQFL-YFDL-IYS-IKDTKLGNY 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 174 AA; 20290 MW; 153533 CN;
                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION: NAME: TUMARKIN, LISA A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: LOS Angeles
CITY: LOS Angeles
CTATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley
                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acid
                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: CLONED Borrelia burgdorferi VIRULENCE TITLE OF INVENTION: PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/0 FILING DATE: 17-JUN-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: P-
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                               Application PC/TUS9507748A
                                                                                                                                                                                                                                                                                                         amino acid
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                                                                                                                                                                                                                                                                                                                    174 amino acids
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Haake, David A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Blanco, David R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Miller, James N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Champion,
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80 Century Park East, Suite 500
                                                                                                                                                                                                                                                                                                                                                              (619) 455-5100
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                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cheryl
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                                                                                                                                                                                                                              Score 99;
Pred. No. |
25; Misma
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Mismatches 32;
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                                                                                                                                                        Sequence 2, Application US/08719124
                                                                                                                                                                                                               US-08-719-124-2
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: HAILE, Ph.D., LISA A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 0741
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5070
TELEPHONE: (619) 678-5099
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                             Sequence 2, Application US/08719124 Patent No. 5854395
                                                                                                                                                                                                                                                                    124 DYLIQLDSDKIDYAEKYGEKARENFEESY 152
                                           GENERAL INFORMATION:
APPLICANT: Champion, Cheryl I.
APPLICANT: Lovett, Michael A.
APPLICANT: Haske, David A.
APPLICANT: Miller, James N.
APPLICANT: Miller, James N.
APPLICANT: Blanco, David R.
TITLE OF INVENTION: CLONED Borrelia burgdorferi VIRULENCE
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                   62 DN-VRVEFKNKDLADKYKDKYVDVFGANY 89
                                                                                                                                                                                                                                                                                                       65 AKAPEIRGSLRKIGIKEN-SVLLDALDVVGFIKSKITTDFLSFIIMNINSLIKGYPNSIF 123
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein PENCE 174 AA; 20290 MW; 153533 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                      PKPDELHKSSKFTGLMENMKVLYDD-NHVSAINVKSIDQFL-YFDL-IYS-IKDTKLGNY 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: The Regents of the University of California TITLE OF INVENTION: CLONED Borrelia burgdorferi VIRULENCE
                                                                                                                                                                                                                                                                                                                                                                              TYPE: ami
TOPOLOGY:
STREET:
CITY: L
STATE:
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FILING DATE: 16-JUN-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                          ADDRESSEE:
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California
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                1880 Century Park East,
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                          Spensley Horn Jubas & Lubitz
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29.2%;
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Pred. No. 8.83e+00
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                  Suite 500
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Matches 26; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 AKAPEIRGSLRKIGIKEN-SVLLDALDVVGFIKSKITTDFLSFIIMNINSLIKGYPNSIF 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (619) 455-51 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    σ
                                                                                                                                        COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Johnson, Howard M. APPLICANT: Pontzer, Carol H. APPLICANT: Griggs, Nathan D. TITLE OF INVENTION: Superanti Superant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
JENCE 174 AA; 20290 MW; 153533 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: PD TELECOMMUNICATION INFORMATION: TELEPHONE: (619) 455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/261,825
FILING DATE: 17-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: TUMARKIN, LISA A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
CURRENT APPLICATION DATA:
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                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                 CITY: Gainesville
STATE: FL
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                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st Street, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: P-38,347
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) 455-5110
NO: 2:
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Pred. No. 8.83e+00;
25; Mismatches 32
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                                                                                                                                                                                                                                                                                                                                                                                               Suite
                                 Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25
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CC APPLICATION NUMBER: US/08/220,378
CC CLINING DATE:
CC CLINING APPLICATION DATA:
CC APPLICATION NUMBER: US 07/941,497
CC RESISTRATION NUMBER: UP126 C1
CC TELEPRORE 09.477-88010
CC THEORAMTION FOR SEQ ID NO. 3:
SEQUENCE CHREACTERSTICS:
CC LENGULE: YEE: Annion acids
CC STRANDEDNESS: Single
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Title: >US-09-150-947-12	Tabular output not generated.	Run on: Thu Apr 20 15:16:39 2000; MasPar time 9.82 Seconds	MPsrch_pp protein - protein database search, using Smith-Waterman algorithm	Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd	(ME)
	res/sec		lgorithm	3	(MT)

Description: Perfect Score: Sequence: (1-239) from US09150947.pep 1763

Scoring table: PAM 150 Gap 11 1 ESQPDPKPDELHKSSKFTGL.....NKMVDSKDVKIEVYLTTKKK 239

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq36 1:geneseqp

Statistics: Mean 32.417; Variance 153.333; scale 0.211

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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42.4	42.4	42.5	42.5	42.6	42.7	42.7	42.7	42.8	42.9	42.9	42.9	43.0	43.1	62.8	64.4	66.7	66.7	97.8	97.8	99.8	100.0	Match L	Query
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Staphylococcus enterot Staphylococcus enterot	Staphylococcus enterot	ס	Staphylococcal enterot			Staphylococcus enterot							S		_	_	Staphylococcal enterot	Staphylococcal enterot		Staphylococcus enterot	Synthetic SEB protein	Description	
6.85e-54 8.39e-54	6.85e-54	4.56e-54	4.56e-54	3.03e-54	2.47e-54	2.02e-54	2.02e-54	1.34e-54	1.09e-54	1.09e-54	1.09e-54	7.29e-55	4.85e-55	5.97e-86	1.86e-88	3.93e-92	3.93e-92	1.44e-141	1.44e-141	9.88e-145	5.29e-145	Pred. No.	

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726	728	730	732	732	737	738	738	739	739	740	740	740	740	742	742	742	745	745	745	745	746
41.2	41.3	41.4	41.5	41.5	41.8	41.9	41.9	41.9	41.9	42.0	42.0	42.0	42.0	42.1	42.1	42.1	42.3	42.3	42.3	42.3	42.3
190	251	251	251	190	190	251	251	251	190	251	251	251	190	190	190	190	251	190	190	190	190
-	_	Н	Н	-	۳	۳	_	_	-	_	1	_	μ	Н	Ľ	٢	_	-	μ	۲	۲
R42011	W59781	W12148	W12146	R42013	R42002	W12147	W12154	W59798	R42001	W59780	W12097	W12150	R42004	R42010	R42006	R41999	W12153	R42003	R41997	R41990	R42005
Staphylococcus enterot	Amino acid sequence of	Streptococcus pyogenes	Streptococcus pyogenes	Staphylococcus enterot	Staphylococcus enterot	Streptococcus pyogenes	Streptococcus pyogenes	Amino acid sequence of	Staphylococcus enterot	Amino acid sequence of	Streptococcus pyogenes	Streptococcus pyogenes	Staphylococcus enterot	Staphylococcus enterot	Staphylococcus enterot	Staphylococcus enterot	Streptococcus pyogenes	Staphylococcus enterot	Staphylococcus enterot	Staphylococcus enterot	Staphylococcus enterot
4.92e-52		2.18e-52	1.45e-52	1.45e-52	5.24e-53	4.28e-53	4.28e-53	3.49e-53	3.49e-53	2.85e-53	2.85e-53	2.85e-53	2.85e-53	1.90e-53	1.90e-53	1.90e-53	1.03e-53	1.03e-53	1.03e-53	1.03e-53	8.39e-54

# ALIGNMENTS

X & O	88888888	8888888	PA PT DR DR PT	RESULT ID W AC W AC S DT 2: DT 2: C S C S C S C S C S C S C S C S C S C S
Query Match 100.0%; Best Local Similarity 100.0%; Matches 239; Conservative	TNF vac of by (es the seq	Exa W64 fra cap PET ant	WPI WPI WPI Ara Ara Ara Ara	ULT W64 W64 23- Syn Ent tox
Matc ocal s	TNF-beta vaccines of T cel by PETs. (especia the pept Sequence	mple 636- gmen able or agon	JUL- DEC- DEC- DEC- DEC- DEC- DEC- DEC- DEC	T 1 W64647 stan W64647; W3-0CT-1998 Synthetic S Enterotoxin toxic shock therapeutic Synthetic.
h Simi 239;	a gers for form	8; 1 W6469 t of of e by a by a ising	W0912944 Al.  O9-TUL-1998  30-DEC-1996; IL-11998. 30-DEC-1996; IL-11998. (YISS) YISSUM RES 6 DEV CO. Arad G, Kaempfer R; WPI; 98-388042/33.  New peptide(s) derived from antagonising toxin-mediated treatment of foxic shock Cau	W64647; W64647; W64647; 23-OCT-1998 Synthetic SEB Enterotoxin Bt toxic shock; therapeutic; therapeutic; cynthetic.
Llard Cor	ines. The trand eli and eli ney can food press can a 239 AA;	Page 57 and Phicipal Page Page Page Page Page Page Page Page	IL I	dard (f: EB p; B; to; to;
1 Lty 1 Serv	The treelici	41; re pe re pe roge ting ting tin-m	7438. -1199 -1199 -139 -100 -100 -100 -100 -100 -100 -100 -10	rst rst rotei SEB; kin-m
100.0%; larity 100.0%; Conservative	pept pept patme ting ting so b	68pp inic pro of pro ledia	DEV	ard; peptide; (first entry) B protein frag B; SEB; pyroge; toxin-mediate; vaccine; food
	ides nt o pro e us ng)	es hexottect	co.	rd; peptide; 239 A (first entry) protein fragment, SEB; pyrogenic e toxin-mediated act vaccine; food pois
Score 1763; DB 1; L Pred. No. 5.29e-145; 0; Mismatches 0;	may f protifecti tecti ed for and t	Example 8; Page 41; 68pp; English.  W64636-W64657 are peptides homologous to the amino acid sequence of fragment of a pyrogenic exotoxin (PET), and derivatives of the peptidespable of eliciting protective immunity against toxic shock induct PET or by a mixture of PETs. Such peptides are also capable of antagonising toxin-mediated activation of T-cells, inhibiting exprosention toxin (PT)-induced mRNA encoded by II-2. IFN-gamma or of pyrogenic toxin (PT)-induced mRNA encoded by II-2. IFN-gamma or of pyrogenic toxin (PT)-induced mRNA encoded by II-2. IFN-gamma or of pyrogenic toxin (PT)-induced mRNA encoded by II-2. IFN-gamma or of pyrogenic toxin (PT)-induced mRNA encoded by II-2. IFN-gamma or of pyrogenic toxin (PT)-induced mRNA encoded by II-2. IFN-gamma or of pyrogenic toxin (PT)-induced mRNA encoded by II-2. IFN-gamma or of pyrogenic toxin (PT)-induced mRNA encoded by II-2. IFN-gamma or of pyrogenic toxin (PT)-induced mRNA encoded by II-2. IFN-gamma or of pyrogenic toxin (PT)-induced mRNA encoded by II-2. IFN-gamma or of pyrogenic toxin (PT)-induced mRNA encoded by II-2. IFN-gamma or of pyrogenic toxin (PT)-induced mRNA encoded by II-2. IFN-gamma or of pyrogenic toxin (PT)-induced mRNA encoded by II-2. IFN-gamma or of pyrogenic toxin (PT)-induced mRNA encoded by II-2. IFN-gamma or of pyrogenic toxin (PT)-induced mRNA encoded by II-2. IFN-gamma or of pyrogenic toxin (PT)-induced mRNA encoded by II-2. IFN-gamma or of pyrogenic toxin (PT)-induced mRNA encoded by II-2. IFN-gamma or of pyrogenic toxin (PT)-induced mRNA encoded by II-2. IFN-gamma or of pyrogenic toxin (PT)-induced mRNA encoded by II-2. IFN-gamma or of pyrogenic toxin (PT)-induced mRNA encoded by II-2. IFN-gamma or of pyrogenic toxin (PT)-induced mRNA encoded by II-2. IFN-gamma or of pyrogenic toxin (PT)-induced mRNA encoded by II-2. IFN-gamma or of pyrogenic toxin (PT)-induced mRNA encoded by II-2. IFN-gamma or of pyrogenic toxin (PT)-induced mRNA encoded by II-2. IFN-gamma or of pyrogenic toxin (PT)-induced mRNA encoded by II-2. IFN-gamma or of py	W09829444-A1.  W09829444-A1.  30-DEC-1998:  IL-11998:  (YISS) YISSUM RES & DEV CO.  Arad G, Kaempfer R;  WPI; 98-388042/33.  New peptide(s) derived from pyrogenic exotoxin - useful for, e.g. antagonising toxin-mediated activation of T cells and prevention from the pyrogenic exotoxin.	T 1 W64647; standard; peptide; 239 AA. W64647; 23-CCT-1998 (first entry) Synthetic SEB protein fragment. Enterotoxin B; SEB; pyrogenic exotoxin; toxic shock; toxin-mediated activation; therapeutic; vaccine; food poisoning. Synthetic.
No.	be upphylive i	ogous (PET (PET Lmmun pep ratio	genic Vatio	otoxi vatic
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DB 1 9e-1 es	to p of ity ity eatm eatm ting	the nd dagain	toxi	ET;
, 15; 16	repair toxin agair ent c ausec tox:	amino eriva nst de als e als ells.	n - (	prote
DB 1; Length 239; 9e-145; ses 0; Indels	re the rect	o aci ative toxic so ca	usefu	PET; protective immunity; T-cell; antagonist; inhib
1 239	lerap liate liate loxic rmfu PET.	d se se of sho	prev	re im onist
0;	eutí d ac sho sho l ef Ant indu	quen the the ck i	r, e enti	mun1 ; in
Gaps	TNF-beta genes. The peptides may be used to prepare therapeutics or vaccines for the treatment of prophylaxis of toxin-mediated activation of T cells and eliciting protective immunity against toxic shock induced by PETs. They can also be used for the treatment of harmful effects (especially food poisoning) and toxic shock caused by PET. Antiserum to the peptides can also be used for alleviating toxic shock induced by PET sequence 239 AA;	Example 8; Page 41; 68pp; English.  W64656-W64657 are peptides homologous to the amino acid sequence of a fragment of a pyrogenic exotoxin (PET), and derivatives of the peptide capable of eliciting protective immunity against toxic shock induced by PET or by a mixture of PETs. Such peptides are also capable of antagonising toxin-mediated activation of T-cells, inhibiting expression of pyrogenic toxin (PT)-induced mNNA encoded by TI-2. TEN-gamma or	W09129444-A1.  109-JUL-1998:  10-DEC-1997; II.0438. 30-DEC-1996; II119938.  (YISS) YISSUM RES & DEV CO. Arad G, Kaempfer R;  WPI; 98-388042/33.  New peptide(s) derived from pyrogenic exotoxin - useful for, e.g. New peptide(s) derived from pyrogenic exotoxin cells and prevention or treatment of foxic shock canced by extravely as	PET; protective immunity; . T-cell; antagonist; inhibitor;
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HNGNQLDKYRSITVRVFEDGKNLLSFDVQTNKKKVTAQELDYLTRHYLVKNKKLYEFNNS 180

HNGNQLDKYRSITVRVFEDGKNLLSFDVQTNKKKVTAQELDYLTRHYLVKNKKLYEFNNS

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                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                           recombinant molecule encoding super:antigen and opt. cytokine or chemokine - controls activity of effector cells (T cells, monocytes, pr natural killer cells) used for gene therapy of cancer ps Example 1: Page 96-97; 131pp; English.

CC A cDNA clone (T4598) codes for staphylococcal enterotoxin B cc (W06737) superantigen. Nucleic acids encoding superantigens (see CC (W06737) superantigen. Nucleic acids encoding superantigen lacking the leader peptide, can be utilised in the gene therapy of cancer. C infectious diseases and immunological disorders. The nucleic acid, coptionally in combination with cytokine or chemokine nucleic acids, controlling the activity of effector cells, such as T-cells, macrophages, monocytes and/or natural killer cells. Localised CC prodn. of an effective but non-toxic amount of encoded proteins controlling safe treatment of the animal.
                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 23
 Staphylococcal
                               R13206 standard; Protein; (239 AA); R13206;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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18-MAY-1995; US-446918.
29-DEC-1995; US-580806.
29-DEC-1995; US-580806.
(NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY MED.
DOW SW, Elmslie RE, Potter TA;
WPI; 97-011857/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enterotoxin B; superantigen; antigen; cytokine; chemokine; T cell;
lymphocyte; monocyte; natural killer cell; gene therapy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus enterotoxin B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W06737 standard;
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                15-OCT-1991 (first entry)
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                                                                                                                           PYETGYIKFIENENSFWYDMMPAPGDKFDQSKYLMMYNDNKMVDSKDVKIEVYLTTKKK
                                                                                                                                                                         HIGNQLDKYRSITVRVFEDGKNLLSFDVQTIKKKVTAQELDYLTRHYLVKKKKLYEFINIS
                                                                                                                                                                                          HNGNQLDKYRSITVRVFEDGKNLLSFDVQTNKKKVTAQELDYLTRHYLVKNKKLYEFNNS
                                                                                                                                                                                                                                     YDNVRVEFKNKDLADKYKDKYVDVFGANYYYQCYFSKKTNDINSHQTDKRKTCMYGGVTE 136
                                                                                                                                                                                                                                                                                                     ESQPDPKPDELHKSSKFTGLMENMKVLYDDNHVSAINVKSIDQFLYFDLIYSIKDTKLGN
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                                                                                                              PYETGY I KF I ENENSFWYDMMPAPGDKFDQSKYLMMY NDNKMVDSKDVK I EVYLTTKKK
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 enterotoxin B
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Pred. No. 9.1
1; Mismatcl
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.88e-145;
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                                                                                                                                                                                                                                                                                                                                     01-JUN-1993; U05213.
01-JUN-1992; US-891718.
(STON/) STONE J L.
(TERM/) TERMAN D S.
Stone JL, Terman DS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus aureus. W09110680-A. W09110680-T. 1991. 17-JAN-1991; U00342. 17-JAN-1990; US-466577. (TERM/) TERMAN D S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Treating cancer with enterotoxin from Staphylococcus aureus administered by IV injection, having same tumoricidal activity as Staphylococcal protein A without potential toxic reactions Disclosure; Fig 1; 74pp; English.

SEB was isolated and purified from S.aureus. It can be used for treating cancer, activating ctoxic mediators and procoagulant systems, augmenting natural killer cell cytotoxicity, etc. The enterotoxin can be administered intravenously, optionally with ibuprofen to attenuate toxic reaction to SEB. Synthetic polypeptides having structural homology to Staphylococcal exotoxins are claimed, provided the homology includes statistically significant sequence homology, alignment of Cysteine residues and similar hydronathy profiles
                                                                                                                                                                                                                                                                                                       Stone
WPI; 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcal enterotoxin SEB.
Staphylococcal enterotoxin; SE; cancer; tumouricidal agent; autoimmune disease; toxicity; Protein A; perfusion system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R45014 standard; protein; (239 AA R45014; 08-JUN-1994 (first entry)
                    Disclosure; Fig 1; 90pp; English.

The sequences given in R45011-21 are Staphylococcal enterotoxins which may be used in the methods of the invention for treating cain a patient. These SEs, and homologues of them, can be used as tumouricidal agents for treating cancers and autoimmune disease. They exhibit tumouricidal activity and toxicity identical to that observed for the Protein A perfusion system. They may be administ
                                                                                                                                                                                                                                       WPI; 93-405418/50.
Use of staphylococcal enterotoxin(s) and homologues - use of staphylococcal enterotoxin or for the treatment of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus W09324136-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similar hydropathy profiles.
See R13203-R13211.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YDNVRVEEKKKDLADKYKDKYVDVEGANYYYQCYFSKKTNDINSHQTDKRKTCMYGGVTE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PYETGYIKFIENENSFWYDMMPAPGDKFDQSKYLMMYNDNKMVDSKDVKIEVYLTTKKK 239
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  injection.
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Pred. No. 1.44e-141;
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Best Local S
Matches 16
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Best Local S
Matches 23
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The sequences given in R45011-21 are Staphylococcal enterotoxins which may be used in the methods of the invention for treating ca in a patient. These SEs, and homologues of them, can be used as tumouricidal agents for treating cancers and autoimmune disease. They exhibit tumouricidal activity and toxicity identical to that observed for the Protein A perfusion system. They may be administ by i.v. injection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Use of staphylococcal enterotoxin(s) and homologues - for treating cancer in a patient or for the treatment of auto-immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stone JL, Terman DS; WPI; 93-405418/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-1993; U05213.
01-JUN-1992; US-891718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus W09324136-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcal enterotoxin; SE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (STON/) STONE J L. (TERM/) TERMAN D S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           autoimmune disease; toxicity; Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-JUN-1994
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                                                                                                     | SPYETGYIKFIENE-NSFWYDMMPAPGDKFDQSKYLMMYNDNKMVDSKDVKIEVYLTTK
                                                                                                                                                                                              YDKVKTELLNEGLAKKYKDEVVDVYGSNYYVNCYFSSK-DNV-GKVTGG-KTCMYGGITK 117
                                                      SSPYETGYIKFIENNGNTFWYDLMPAPGDKFDQSKYLMMYNDNKTVDSKSVKIEVHLTTK 237
                                                                                                                                                                            YDNVRVEFKNKDLADKYKDKYVDVFGANYYYQCYFSKKTNDINSHETDKRKTCMYGGVTE
                                                                                                                                                                                                                                                                                                                                                                                         injection.
e 239 AA;
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llarity 97.9%;
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                                                                                                                                                                                                                                                                                                                      41; Mismatches
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Pred. No. 1.44e-141;
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                                                                                                                                                                                                                                                                                                                                      1176; DB 1;
No. 3.93e-92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; perfusion system.
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Best Local S
Matches 16
                                                                   Staphylococcus aureus. W09324136-A. 09-DEC-1993.
                                                                                                                    R45016;
08-JUN-1994 (first entry)
Staphylococcal enterotoxin SEC3.
Staphylococcal enterotoxin; SE;
autoimmune disease; toxicity; Pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     treating cancer, activating cytokine mediators and procoagulant systems, augmenting natural killer cell cytotoxicity, etc. The enterotoxin can be administered intravenously, optionally with ibuprofen to attenuate toxic reaction to SEC1. Synthetic polypeptides having structural homology to Staphylococcal exotoxins are claimed, provided the homology includes statistically structural homology includes statistically statisticant sequence homology, alignment of Cysteine residues and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Treating cancer with enterotoxin from Staphylococcus aureus administered by IV injection, having same tumoricidal activity as Staphylococcal protein A without potential toxic reactions Disclosure; Fig 1; 74pp; English.

SECI was isolated and purified from S.aureus. It can be used for the state of the st
01-JUN-1993; U05213.
01-JUN-1992; US-891718.
(STON/) STONE J L.
(TERM/) TERMAN D S.
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17-JAN-1990; US-466577.
(TERM/) TERMAN D S.
Terman DS;
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R13207 standard;
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R13203-R13211.
uence 239 AA;
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                                                                                                                                                                                                             l6 standard; protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                          HNGNQLDK-Y-RSITVRVFEDGKNLLSFDVQTNKKKVTAQELDYLTRHYLVKNKKLYEFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YDNVRVEFKNKDLADKYKDKYVDVFGANYYYQCYFSKKTNDINSHETDKRKTCMYGGVTE
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160; Conser
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Pred.
41; M
                                                                                                                         Protein A; perfusion system
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                                                                                                                                         cancer; tumouricidal agent;
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1. No. 3.93e-92;
1. Tentches 34;
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Length Indels

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Gaps

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Best Local S
Matches 15
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Best Local
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                                                                                                                                                                                                                                                                                       Treating cancer with enterotoxin from Staphylococcus aureus administered by IV injection, having same tumoricidal activity as Staphylococcal protein A without potential toxic reactions isclosure; Fig 1; 74pp; English.

SEC3 was isolated and purified from S.aureus. It can be used for treating cancer, activating cytokine mediators and procoagulant systems, augmenting natural killer cell cytotoxicity, etc. The enterotoxin can be administered intravenously, optionally with buprofen to attenuate toxic reaction to SEC3. Synthetic polypeptides having structural homology to Staphylococcal exotoxins are claimed, provided the homology includes statistically significant sequence homology, alignment of Cysteine residues and significant sequence homology, alignment of Cysteine residues
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The sequences given in R45011-21 are Staphylococcal enterotoxins which may be used in the methods of the invention for treating c in a patient. These SEs, and homologues of them, can be used as tumouricidal agents for treating cancers and autoimmune disease. They exhibit tumouricidal activity and toxicity identical to the observed for the Protein A perfusion system. They may be adminiby i.v. injection.
                                                                                                                                                                                                                    similar hydropathy profiles.
See R13203-R13211.
Sequence 238 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus aureus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Terman DS;
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17-JAN-1990; US-466577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9110680-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-OCT-1991 (first entry)
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155; Conse
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156; Conser
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39; M
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d. No. 5.97e-86;
Mismatches 40;
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. No. 1.86e-88;
Mismatches 37;
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Best Local :
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28-JAN-1993; U00839.
28-JAN-1992; US-827540.
(NAJE-) NAT JEWISH CENT I
KAPPLET JW, MAITACK P;
WPI; 93-320314/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents the Staphylococcus enterotoxin B (SEB) super antigen (SAg). Mutant versions of this sequence generated by random mutation by PCR, may be used to modify the T-cell response elicited by an antigen, by interacting with specific Vbeta elements of the T-cell receptors. This T-cell response modulation may be useful in a wide variety of autoimmune diseases, where self-reactive T-cells may be activated by SAg that bind to particular Vbeta types. Sequence 190 AA;
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R41989;
21-APR-1994 (first entry)
Staphylococcus enterotoxin B.
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Disclosure; Fig 3; 54pp;
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Pred. No. 4.85e-55;
29; Mismatches 48
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R42007 standard; protein; 190 R42007; 21-APR-1994 (first entry)

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Best Local S
Matches 11
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05-AUG-1993.
28-JAN-1993; U00839.
28-JAN-1992; US-827540.
(NAJE-) NAT JEWISH CENT I
KAPPLE: JW, MATTACK P;
WPI; 93-320314/40.
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28-JAN-1992; US-827540.
(NAJE-) NAT JEWISH CENT I
KAPPLEY JW, MATTACK P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequences given in R41990-2013 are mutant versions of the Staphylococcus enterotoxin B (SEB) super antigen (SAg). These mutant generated by random mutation by PCR, may be used to modify the T-cel response elicited by an antigen, by interacting with specific Vbeta elements of the T-cell receptors. This T-cell response modulation may be useful in a wide variety of autoimmune diseases, where self-reactive T-cells may be activated by SAg that bind to particular
                                                                                                                                                                                                                                                                                                                                               Staphylococcus; enterotoxin B; SEB; super antigen; SAg; receptor;
                                                                                                                                                                                                                                                                                                                                                                                                  R42012;
21-APR-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Preventing or treating toxic on mew modified or mutated super
                                                                                                                                                                                        region
                                                                                                                                                                                                                                       region
                                                                                                                                                                                                                                                                                  Staphylococcus
                                                                                                                                                                                                                                                                                                           autoimmune disease
                                                                                                                                                                                                                                                                                                                              random mutation; PCR; modify; T-cell; response;
                                                                                                                                                                                                                                                                                                                                                                                                                                              R42012 standard; protein; 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 not T-cell activation
Disclosure; Fig 3; 54pp; English.
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Staphylococcus; enterotoxin B; SEB; super antigen; SAg; receptor; random mutation; PCR; modify; T-cell; response; antigen; Vbeta el
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vbeta types
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larity 58.9%;
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162. .1
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                                                IMMUNOLOGY & RESPIRATORY
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Pred.
30; M
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No. 7.29e-55;
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28-JAN-1993; U00839.

28-JAN-1992; US-827540.

(NAJE-) NAT JEWISH CENT I

Kappler JW, Marrack P;

WPI; 93-320314/40.
                                                                                                                          Disclosure: Fig 3: 54pp: English.

The sequences given in R41990-2013 are mutant versions of the Staphylococcus enterotoxin B (SEB) super antigen (SAg). These mutants generated by random mutation by PCR, may be used to modify the T-cell response elicited by an antigen, by interacting with specific vbeta elements of the T-cell receptors. This T-cell response modulation may be useful in a wide variety of autoimmune diseases, where self-reactive T-cells may be activated by SAg that bind to particular
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R41993;
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new modified or mutated super antigen which induces antib
not T-cell activation
Disclosure; Fig 3; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
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                                                                                                                  Vbeta types
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l Similarity 58.9%;
l12; Conservative
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162. .]
/note=
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97. .157
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Score
Pred.
30; M
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Pred. No. 1.09e-54;
30; Mismatches 48
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Mismatches
                        756; DB 1;
No. 1.09e-54;
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                                           Length 190
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Best Local
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The sequences given in R41990-2013 are mutant versions of the Staphylococcus enterotoxin B (SEB) super antigen (SAg). These mutants generated by random mutation by PCR, may be used to modify the T-cell response elicited by an antigen, by interacting with specific Vbeta elements of the T-cell receptors. This T-cell response modulation may be useful in a wide variety of autoimmune diseases, where self-reactive T-cells may be activated by SAg that bind to particular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-JAN-1992; US-827540.
(NAJE-) NAT JEWISH CENT
Kappler JW, Marrack P;
WPI; 93-320314/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus enterotoxin B mutant BC-88.
Staphylococcus; enterotoxin B; SEB; super antigen; SAg; receptor; random mutation; PCR; modify; T-cell; response; antigen; Vbeta el
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Preventing or treating toxic effects of super antigens - by admin. new modified or mutated super antigen which induces antibodies but
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05-AUG-1993.
28-JAN-1993; U00839
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21-APR-1994 (first entry)
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Local Similarity 58.9%;
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97. .157
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                                                                                                                                                                                                                                                                                                                                                                                                                       Score 756;
Pred. No. 1.
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1.09e-54;
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28-JAN-1993; U00839.

28-JAN-1992; US-827540.

(NAJE-) NAT JEWISH CENT I

Kappler JW, Marrack P;

WPI; 93-320314/40.
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Disclosure; Fig 3; 54pp; English.
The sequences given in R41990-2013 are mutant versions of the Staphylococcus enterotoxin B (SEB) super antigen (SAg). These mutants generated by random mutation by PCR, may be used to modify the T-cell response elicited by an antigen, by interacting with specific Vbeta elements of the T-cell receptors. This T-cell response modulation may be useful in a wide variety of autoimmune diseases, where self-vective T-cells may be activated by SAg that bind to particular
                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus; enterotoxin B mutant BA-15. Staphylococcus; enterotoxin B; SEB; super antigen; SAg; receptor;
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R42000;
21-APR-1994 (first entry)
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Staphylococcus; enterotoxin B; SEB; super antigen; SAg; receptor; random mutation; PCR; modify; T-cell; response; antigen; Vbeta element;
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R41992;
21-APR-1994 (first entry)
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162. .186
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162. .:
                                                                                                                                                                                          Location/Qualifiers 97. .157
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Pred. No. 1.34e-54;
31; Mismatches 48
                                                                                                                                                                                                                                                                                                                                             T-cell; response;
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PR 28-JAN-1992; US-877540.

PA (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.

PA (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATO
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Thu Apr 20 15:08:07 2000; MasPar time 15.27 Seconds 467.552 Million cell updates/sec

Tabular output not generated.

Title: >US-09-150-947-12 (1-339) from US09150947.pep 1763 1 ESOPDBK DRTT....

Description: Perfect Score: Sequence: ESQPDPKPDELHKSSKFTGL.....NKMVDSKDVKIEVYLTTKKK 239

Scoring table: PAM 150 Gap 11

Searched: 82229 seqs, 29864866 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot38 1:swissprot

Statistics: Mean 47.318; Variance 95.221; scale 0.497

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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## ALIGNMENTS

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"Crystal structure of microbial superantigen staphylococcal
enterotoxin B at 1.5-A resolution: implications for superan
recognition by MHC class II molecules and T-cell receptors.
J. Mol. Biol. 277:61-79(1998).
"THE PROPERTY OF THE INTOXICA ENTEROTOXINS CAUSE THE INTOXICA
                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
PFAM; PF01123; Stap_Strp_toxin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                  SEQUENCE
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MEDLINE; 83213327.

SCHMIDT J.J., SPERO L.;

SCHMIDT J.J., SPERO L.;

"The complete amino acid sequence of staphylococcal enterotoxin
J. Biol. Chem. 258:6300-6306(1983).

-!- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
STAPHYLOCOCCAL FOOD POISONING SYNDROME.

-!- SIMILARITY: THE DIFFERENT S.AUREUS ENTEROTOXINS AND S.PYOGEN
PYROGENIC EXOTOXINS ARE ALL RELATED.
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PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
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BOHACH G.A., SCHLIEVERT P.M.;

"Nucleotide sequence of the sequence of the
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SEQUENCE
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-i- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HOVDE C.J., HACKETT S.P., BOHACH G.A.;
"Nucleotide sequence of the staphylococcal enterotoxin C3
sequence comparison of all three type C staphylococcal
enterotoxins.";
                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00277; STAPH_STREP_TOXIN_1; PROSITE; PS00278; STAPH_STREP_TOXIN_2; PFAM; PF01123; Stap_Strp_toxin; 1. Enterotoxin; Toxin; Signal; Superantige SIGNAL 1 27
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Bacillus/Staphylococcus
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SIMILARITY: THE DIFFERENT S.AUREUS ENTEROTOXINS
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                                                                                                                                               ESQPDPKPDELHKSSKFTGLMENMKVLYDDNHVSAINVKSIDQFLYFDLIYSIKDTKLGN 60
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Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                            dissimilarity.";
J. Mol. Biol. 269:270-280(1997).
-I- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
                                                                                                                                                                                                                                                                                                                MEDLINE; 97334373.
SCHAD E.M., PAPAGEORGIOU A.C., SVENSSON L.A., ACHARYA K.R.; "A structural and functional comparison of staphylococcal "A structural and C2 reveals remarkable similarity and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Crystal structure of the superantigen enterotoxin Staphylococcus aureus reveals a zinc-binding site." Structure 3:769-779(1995).
SEQUENCE
                                                                                                                                                                                                                   PIR; A60114; A60114.
                                                                                                                                                                                                                                                                                                                                                                                                                                        enterotoxins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BOHACH G.A., SCHLIEVERT P.M.; "Conservation of the biologically active enterotoxins C1 and C2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND MEDLINE; 89277549.
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                                                                                                                                                                                  PDB; 1STE; 23-DEC-96.
PDB; 1SE2; 08-MAR-96.
                                                                                                                                                                                                                                                                                                                                                                                             COMPARISON OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWAMINATHAN
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BREHM R.D., TRANTER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
                                                                                                          SIGNAL
                                                                                                                          Enterotoxin;
                                                                                                                                         PFAM; PF01123;
                                                                                                                                                                                                                                                                                                                                                                                                                              Nat. Struct.
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                                                                                                                                                      PROSITE;
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                                                                                                                                                                                                                                                  STAPHYLOCOCCAL FOOD POISONING SYNDROME SIMILARITY: THE DIFFERENT S.AUREUS ENT
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                                                                                                                                    PS00277; STAPH_STREP_TOXIN_1;
PS00278; STAPH_STREP_TOXIN_2;
01123; Stap_Strp_toxin; 1.
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(Rel. 28, Last sequence update)
(Rel. 38, Last annotation update)
TYPE C-2 PRECURSOR (SEC2).
                                                                                                                         Toxin;
                                                                                                                                                                                                                                                                                                                                                                                                                             Biol.
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                                                                                                             Signal;
27
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                                                                                                                         Superantigen; Zinc;
                             ZINC.
                                                                                             ENTEROTOXIN TYPE C-2
A115FD37 CRC32;
                                                                                                                                                                                                                                     RELATED
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                                                                                                                                                                                                                                                                                                                                                                                             SEC2
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                                                                                                                         3D-structure
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                                                     the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
      EMBL;
PIR; PIR;
                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE; 86284313.
                                                                                                                                                                                                                                                                                                                                                       WEEKS C.R., FERRETTI J.J.;
"Nucleotide sequence of the type (erythrogenic toxin) gene from
                                                                                                                                                                                                                                                   JOHNSON L.P., L'ITALIEN J.J., SCHLIEVERT P.M.;
"Streptococcal pyrogenic exotoxin type A (scarlet related to Staphylococcus aureus enterotoxin B.";
Mol. Gen. Genet. 203:354-356(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus pyogenes Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                    Infect.
                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus.
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                                                                                                                                                                                             Gen. Genet. 203:354-356(1986).

DISEASE: THE STREPTOCOCCAL PYROGENIC TOXINS A, B, AND C ARE THE CAUSATIVE AGENTS OF THE SYMPTOMS ASSOCIATED WITH SCARLET FEVER, HAVE BEEN ASSOCIATED WITH STREPTOCOCCAL TOXIC SHOCK-LIKE DISEASE AND MAY PLAY A ROLE IN THE EARLY EVENTS OF RHEUMATIC
                                                                                                                                                                    MISCELLANEOUS: THIS TOXIN SEEMS TO SIMILARITY: THE DIFFERENT S.AUREUS
      A26152;
S29659;
                                                                                                                                                         PYROGENIC EXOTOXINS ARE ALL
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                           U40453; AAC48868.1;
X03929; CAA27568.1;
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990 (Rel. 13, Last sequence update)
998 (Rel. 37, Last annotation update)
998 (Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                        FROM N.A.
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       A26152.
S29659.
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com Streptococcus
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ETXD_STAAU
P20723;
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SIGNAL
                "The crystal structure of staphylococcal entero In2+mediated homodinerization.";
EMBO J. 15:6832-6840(1996).
-i- SUBUNIT: HOMODIMER; ZINC-DEPENDENT.
-i- DISEASE: STAPHYLOCOCCAL ENTEROTOCIONES CAUSE STAPHYLOCOCCAL FOOD POISONING SYNDROME.
-i- SIMILARITY: THE DIFFERENT S.AUREUS ENTEROTO
                                                                                                                                                                                                         Staphylococcus aureus.
                                                                                              SEQUENCE FROM N.A., STRAIN-ATCC 23235; MEDLINE; 97157473.
                                                                                                                                         enterotoxin D.
                                                                                                                                                           BAYLES
                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE; 89359112.
                                                                                                                                                                                            Bacillus/Staphylococcus
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                                                                                      SUNDSTROEM M., ABRAHMSEN
                                                                                                                                                  BAYLES K.W., IANDOLO J. "Genetic and molecular
                                                                                                                                                                                                      Bacteria;
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                                                                             OHLSTEN M.
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                                                                                                                                  Bacteriol.
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                                                                                                                                  171:4799-4806(1989).
         EXOTOXINS
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D PRECURSOR (SED).
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STAPH_STREP_TOXIN_2;
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VT -> MK (IN REF. 2).

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H -> Q (IN REF. 2).

S -> N (IN REF. 2).

NLQNIYFLYEGDP -> TFKIYIFFMRV
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Pred. No. 1.
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01-JAN-1990
15-JUL-1999
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"Nucleotide sequence of the ty
J. Bacteriol. 170:34-41(1988).
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MEDLINE; 87222293.
HUANG I.-Y., HUGHES
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  SCHAD E.M., ZAITSEVA I., SCHLIEVERT P.M., OHLENDO
                                                                                                                                                                                                                                                                                            MEDLINE; 88086892
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                                                                                                                                                                                                                                                                                                                                                                          Bacillus/Staphylococcus
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HSSP; P13163; 1SXT.
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                                                                                                    -Y., HUGHES J.L., BERGDOLL M.S., SCHANT:
e amino acid sequence of staphylococcal
Chem. 262:7006-7013(1987).
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ZAITSEV V.N., DOI
RF D.H., SVENSSON
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53; N
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                                                                                                                                                                                                                                                  type A staphylococcal enterotoxin gene.";
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Pred. No. 2.16e-54
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CONFLICT
SEQUENCE
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METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                   "A Structural and functional comparison of staphylococcal enterotoxins A and C2 reveals remarkable similarity and dissimilarity.";

J. Mol. Biol. 269:270-280(1997).
                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Crystal structure of the superantigen staphylococcal enterotoxin type A."; EMBO J. 14:3292-3301(1995). [4]
                                                                                                                                                           METAL
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PDB; 1SEA; 15-OCT-95.
PDB; 1SXT; 19-NOV-97.
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Nat. Struct. B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The Co-crystal structure of staphylococcal enterotoxin type A with 2n2+ at 2.7-A resolution. Implications for major histocompatibility complex class II binding.";
J. Biol. Chem. 271:32212-32216(1996).
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                                                                                                                                                                      METAL
                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                         Enterotoxin;
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                                                                                                                                                                                                               SIGNAL
 83
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                                                                                                                                                                                                                                                                                                                                         send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                 A28664; A28664.
A29566; A29566.
FKNKDLADKYKDKYVDVFGANYYYQCYFSKKTNDINSHETDKRKTCMYGGVTEHNGNQLD 127
                                                   Struct. Biol. 2:680-686(1995)
                    FDSKDIVDKYKGKKVDLYGAYYGYQC-----AGG--T--PNK-TACMYGGVTLHDNNRLT 144
                                        ELHKSSKFTGL-MENMK-VLYDDNHVSAINVKSIDQFLYFDLIYSIKDTKLGNYDNVRVE
                                                                                            Similarity
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                                                                                 Score 375; DB 1;
Pred. No. 2.55e-47;
56; Mismatches 77
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                                                                                                                                     ZINC.
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D08631B2
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CRC32;
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                                                                                  77;
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                                                                                                      Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                    BY A BACTERIOPHAGE XINS AND S.PYOGENES
                                                                                                                                                                                                                         3D-structure
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01-JAN-1990
15-JUL-1999
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Staphylococcus aureus.
Bactleria; Firmicutes; Bacillus/Clostridium group;
Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                     PROSITE; PS00277; STAPH_STREP_TOXIN_1; PROSITE; PS00276; STAPH_STREP_TOXIN_2; PFAM; PF01123; Stap_Strp_toxin; 1.
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P12993;
                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               enterotoxins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Cloning and nucleotide sequence of the type E staphylococcal enterotoxin gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENTEROTOXIN
                                                                                                                                                                                                                                           Enterotoxin; Toxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWAMINATHAN S., FUREY W.F. JR., PLETCHER J., "Residues defining V beta specificity in sta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWAMINATHAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3D-STRUCTURE MODELING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            .. Struct. Biol. 2:680-686(1995).
DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE I STAPHYLOCOCCAL FOOD POISONING SYNDROME.
SIMILARITY: THE DIFFERENT S.AUREUS ENTEROTOXINS PYROGENIC EXOTOXINS ARE ALL RELATED.
                                                                                                                   DLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTGHPWYNDLLVD
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         EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 204
                                   FKNKDLADKYKDKYVDVFGANYYYQCYFSKKTNDINSHETDKRKTCMYGGVTEHNGNQLD 127
                                                              LGSKDATNKYKGKKVDLYGAYYGYQC-----AGG--T--PNK-TACMYGGVTLHDNNRLT 144
                                                                                          ELHKSSKFT-GLMENMK-VLYDDNHVSAINVKSIDQFLYFDLIYSIKDTKLGNYDNVRVE 67
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                                                                                                                                               79;
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257 /
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(Rel. 13, Last sequence update)
(Rel. 38, Last annotation updat
TYPE E PRECURSOR (SEE).
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                                                                                                                                               Conservative
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                                                                                                                                              Pred.
56; N
                                                                                                                                                            Score 329; DB 1;
Pred. No. 1.15e-38;
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                                                                                                                                                                                                    ENTEROTOXIN TYPE 88BA67C3 CRC32;
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P13380;
01-JAN-1990
                                                                                                                                                                                                                                     PIR;
                                                                                                                                                                                                                                                          EMBL; M35514; AAA27017.1; ALT_SEQ.
EMBL; M97156; AAB59091.1; -.
EMBL; M97157; AAB59092.1; -.
                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-i- DISEASE: THE STREPTOCOCCAL PYROGENIC TOXINS A, B, AND C ARE THE CAUSATIVE AGENTS OF THE SYMPTOMS ASSOCIATED WITH SCARLET FEVER, HAVE BEEN ASSOCIATED WITH STREPTOCOCCAL TOXIC SHOCK-LIKE DISEASE AND MAY PLAY A ROLE IN THE EARLY EVENTS OF RHEUMATIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 97397352.

ROUSSEL A., ANDERSON B.F., BAKER H.M., FRASER J.D., BAKER E.N.;
"Crystal structure of the streptococcal superantigen SPE-C:
"Crystal structure of the streptococcal superantigen SPE-C:
"Crystal structure of the streptococcal superantigen SPE-C:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Molecular population genetic evidence of alleles of the pyrogenic exotoxin C gene (clones of Streptococcus pyogenes."; Infect. Immun. 60:3513-3517(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REVISIONS TO 21-26.
STRAIN=T18P / MGAS 1585;
MEDLINE; 92363541.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GOSHORN S.C., SCHLIEVERT P.M.; "Nucleotide sequence of streptococcal pyrogenic exotoxin type C."; Infect. Immun. 56:2518-2520(1988).
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                                                         SIGNAL
                                                                                    PROSITE; PS00277; STAPH_STREP_TOXIN_1; PROSITE; PS00278; STAPH_STREP_TOXIN_2; PFAM; PF01123; Stap_Strp_toxin; 1.
Toxin; Signal; 3D-structure.
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STRAIN-T18P / MGAS
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   SEQUENCE
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1585;
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      EXOTOXIN TYPE C. 524BB55D CRC32;
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Best Local :
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SEGHEZZI W., MEILI C., RUFFINER R., KUENZI R., FIECHTER A.;
                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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15-DEC-1998 (Rel. 37
CYTOCHROME P450 52A8
                                                                                                                 PROSITE; PS00086; CYTOCHROME_P450; 1.
PFAM; PF00057; P450; 1.
Electron transport; Oxidoreductase; Monooxygenase;
BINDING 464 HEME (BY SIMILARITY).
SEQUENCE 517 AA; 59525 MW; D851204F CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Candida tropicalis
Eukaryota; Fungi; 1
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                                                                                                                                                                                          EMBL; Z13012; CAA78356.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Candidaceae;
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 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          114 MYGGVTEHNGNQLDKYRSI-TVRVFEDGKNLLSFDVQTNKKKVTAQELDYLTRHYLVKNK 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113 IYGGITPAQNNKVN-HKLLGNLFISGESQQNLNNKIILEKDIVTFQEIDFKIRKYLMDNY 171
                                               189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              231 EVYL 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            173 KLYEFNNSPYETGYIKFIENENSF-WYDMMPAPGDKFDQSKYLMMYNDNKMVDSKD-VKI 230
                       36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10
                                                                                                                                                                                                                                                                                                            INDUCTION: BY VARIOUS ALKANES.
SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
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                       INVKSIDQFLYFDLIYSIKDTKLGNYDNVRVEFKN-KDLADKY-KDK-YVDV--FGANYY
                                                                                                                                                                              S22974;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KIYD-ATSPYVSGRIEIGTKDGKHEQIDLFDSPNEG-TRSDIFAKYKDNRIINMKNFSHF 229
                                             FTVDSATEFLFGESVHSLKDETIGSYQDD-IDFVGRKDFAESFNKAQEYLAIRTLVQDFY 247
 248
                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25, Last sequence update)
37, Last annotation update)
2A8 (EC 1.14.14.1) (CYPLIIA8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ascomycota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25, Created)
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Pred. No. 6.04e-10;
37; Mismatches 49
                                                                     20;
                                                                                Score 112;
Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hemiascomycetes;
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                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               517
                                                                                DB 1;
.24e-02;
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                                                                                          Length 517
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Best Local
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Q12387;
Q1-NOV-1997
Q1-NOV-1997
                                                                                                                                                                                           Q04711;
01-NOV-1997
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U36382; AAA79781.1; -.
EMBL; U54799; AAB00196.1; -.
EMBL; Z74818; CAA99086.1; -.
SGD; L0002975; DEC1.
SEQUENCE 796 AA; 92808 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a copyreen the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TZERMIA M., KATSOULOU C., ALEXANDRAKI D.;
"Sequence analysis of a 33.2 kb segment from the chromosome XV reveals eight known genes and ten not frames including homologues of ABC transporters, phosphatases and human expressed sequence tags.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEC1 OR MDM20 OR YOL076W.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Hemiascomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997
DEC1 PROTEIN
                                                Eukaryota; Fungi; A
Saccharomycetaceae;
                                                                         Saccharomyces cerevisiae (Baker's yeast). Eukaryota; Fungi; Ascomycota; Hemiascomyc
                                                                                                                         TY1B OR YML044W OR YM9827.08
                                                                                                                                           01-NOV-1997 (Rel. 35, C
01-NOV-1997 (Rel. 35, L
15-DEC-1999 (Rel. 39, L
TRANSPOSON TY1 PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE; 97321807.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. HERMANN G.J., SHAW J.M.; Submitted (APR-1996) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. KINGSBURY T.J., HC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomycetaceae;
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                    YME4_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yeast 13:583-589(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                  103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KFKQSPGK-FDYNKLLEEPYGLKGTTITGDTRSLEFL-HNFFVELGK-YDEALHVYERGN 102
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NY-1997 (Rel. 35, Last sequence update)
Y-1997 (Rel. 35, Last annotation updat
PROTEIN (MDM20 PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                  IKFIENENSF-WYDMMPAPGDKFDQ 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                KYRSITVRVFEDGKNLL-SFDVQTNKKKVTAQELDYLTRHYLVKNKKLYEFNNSPYETGY 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h 6.0%;
Similarity 22.4%;
19; Conservative
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cetaceae; Saccharomyces
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                                                                      Ascomycota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92808 MW;
                                                  Saccharomyces
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                                                                                                                                                                                              sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 105; DB 1;
Pred. No. 2.56e-01;
24; Mismatches 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL/GenBank/DDBJ
                                                                      Hemiascomycetes;
                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                    1328 AA
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                                                                         Saccharomycetales;
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RESULT ACCOUNTS OF THE BEAUTY 
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Best Local Similarity
Carreles 20; Conserv
~ B
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Best Local :
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                             1009 LNANKKIITTLKKQYDTKIINLGESDNEIQYDIL-GLEIKYQRGKYMKLGMENSLTE-KI 1066
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                                                                                                                                                                                                                                                                                                                     ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-S288C / AB972;
CONNOR R., CHURCHER C., BARRELL B.G., RAJANDREAM M.A.;
SUDMILTED (FEB-1995) to the EMBL/GenBank/DDBJ databases.
-I- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY U23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOY-1997 (Rel. 35, Created)
01-NOY-1997 (Rel. 35, Last sequence up
15-DEC-1999 (Rel. 39, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ODELL C., BOWMAN S., BARRELL B.G., RAJANDREAM M.A.;
Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY U23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Hemiascomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TY1B OR YML039W OR YM8054.04
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PROSITE; PS00141; ASP_PROTEASE; 1.
                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                    Aspartyl
                                                                                                                                                                                                                                                                                                                                                                                                                                     Transposable element; Hypothetical protein; Hydrolase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00141; ASP_PROTEASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Z48430; CAA88330.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSPOSON TY1 PROTEIN B
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                                                                                                            Local Similarity
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Pred. No. 1.92e-01;
23; Mismatches 25; Indels
                                                                                                    Score 106; DB 1;
Pred. No. 1.92e-01;
23; Mismatches 25
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Q04670;
MEDLINE; 86205247.

WARMINGTON J.R., ANWAR R., NEWLON C.S., WARING R.B., DAVIES INDGE K.J., OLIVER S.G.;
"A 'hot-spot' for Ty transposition on the left arm of yeast chromosome III.";
                                                                                                                                                      YCB9_YEAST STANDARD; PRT; 13
P25384;
01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence up
15-DEC-1998 (Rel. 37, Last annotation
TRANSPOSON TY1-17 PROTEIN B.
TY1B OR YCL019W OR YCL19W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-S288C / AB972;
DEVLIN K., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A.;
SUDMITTED (MAY-1995) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY U23.
                                                                                                                         Saccharomyces cerevisiae (Baker's yeast). Eukaryota; Fungi; Ascomycota; Hemiascomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00141; ASP_PROTEASE; 1. Transposable element; Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restuse by non-profit institutions as long as its content
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01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation updat
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                                                                                                          Saccharomycetaceae;
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1328 AA;
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Pred. No. 1.92e-01;
23; Mismatches 25
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Search completed: Thu Apr 20 15:09:35 2000 Job time: 88 secs.
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Best Local Similarity 29.2%;
Matches 21; Conservative
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EMBL; X59720; E264443; -.
PIR; B23496; B23496.
PIR; S19345; S19345.
Transposable element; Hypothetical protein; Hydrolase; Aspartyl protease; ATP-binding.
NP_BIND 123 1230 ATP (POTENTIAL).
SEQUENCE 1347 AA; 154069 MW; 71FC7229 CRC32;
                                                                                                                                                                                                                                                                     1086 PKLNVPLNPKGK 1097
                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SUBMITTED (MAR-1992) to the EMBL/GenBank/DDBJ databases.
-I- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY U23.
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MEDLINE; 86041864.
MEDLINE; 86041864.
MERMINGTON J.R., WARING R.B., NEWLON C.S., INDGE K.J., OLIVER S.G.;
"Nucleotide sequence characterization of Ty 1-17, a class II
transposon from yeast.";
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[2]
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Apr 20 15:13:54 2000; MasPar time 17.90 Seconds 629.702 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: Title:

>US-09-150-947-12 (1-239) from USO9150947.pep 1763 1 ESQPDPKPDELHKSSKFTGL.....NKMYDSKDVKIEVYLTTKKK 239

Scoring table: PAM 150 Gap 11

Searched: 142080 segs, 47172406 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: pir62 1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 46.393; Variance 108.813; scale 0.426

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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## ALIGNMENTS

#cross-referents #contents REFERENCE #authors #journal #title	##experimen REFERENCE #authors #journal #title	##molecule ##residues	#authors #journal #title #cross-referent	##molecule_type DNA ##residues 1-2 ##cross-references ##experimental_sour REFERENCE A92065	REFERENCE # journal # title # cross references to the state of the sta	RESULT 1 ENTRY TITLE ORGANISM DATE ACCESSIONS
#cross-references MUID:71007901 #contents annotation; chymotryptic peptides #ERENCE A92063 #authors Huang, I.Y.; Bergdoll, M.S. #authors Holl. Chem. (1970) 245:3493-3510 #fournal J. Biol. Chem. (1970) a5:3493-3510 #title The primary structure of staphylococcal enterotoxin B. I. #solation, composition, and sequence of tryptic peptides from oxidized entero-toxin B.	##experimental_source strain S-6 A92064 A92064 Thors Huang, I.Y.; Bergdoll, M.S. Urnal J. Biol. Chem. (1970) 245:3511-3517 The primary structure of staphylococcal enterotoxin B. II.	##molecule_type protein 28-55,'NND',59-68,'NE',71,'FDLIYL',78-117,119-127,'N', 129,'D',131-132,'ENT',136-148,'GN',151-156,'Y', 157-184,'EQ',187-232,'N',234-245,'ND',248-266 ##label	authors Huang, I.Y.; Bergdoll, M.S.  Journal J. Biol. Chem. (1970) 245:3518-3525  The primary structure of staphylococcal enterotoxin B. III.  The cyanogen bromide peptides of reduced and aminoethylated enterotoxin B, and the complete amino acid sequence.  cross-references MUID:71007902  accession A92065	##molecule_type DNA 1-266 ##label JON ##cross-references EMBL,M11118; NID:g152999; PIDN:AAA88550.1; ##experimental_source strain S6 NCE A92065	#AUTHORS JONES, C.L.; Khan, S.A. #authors Jones, C.L.; Khan, S.A. #journal J. Bacteriol. (1986) 166:29-33 #title Nucleotide sequence of the enterotoxin B gene from Staphylococcus aureus. #cross-references MUID:86168029 #acression S27360	ENSAB6 #type complete enterotoxin B precursor - Staphylococcus aureus #formal_name Staphylococcus aureus 24-Apr-1984 #sequence_revision 15-Oct-1996 #text_change 18-Jun-1999 \$27366; A92065; \$27240; A01815

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#title
enterotoxin C-1.
#cross-references MUID:83213327
#accession A01816
                                                                                                                                                                                                                                                                                                                               #authors Bohach, G.A.; Schlievert, P.M.
#journal Mol. Gen. Genet. (1987) 209:15-20
#title Nucleotide sequence of the staphylococcal enterotoxin
and relatedness to other pyrogenic toxins.
#cross-references_MUID:88038352
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Dunnery, D.A.; Bergdoll, M.S.
#journal Biochemistry (1965) 4:1011-1016
#title Purification of staphylococcal enterotoxin
#cross-references MUID:66035792
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15-Nov-1984 #sequence_revision 05-Jan-1996
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                                                                                      A01816
Schmidt, J.J.; Spero, L.
J. Blol. Chem. (1983) 258:6300-6306
The complete amino acid sequence of
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##cross-references GB:X51661; NID:g46570; PIDN:CAA35972.1; PID:g46571
#FICATION #superfamily enterotoxin B
#length 266 #molecular-weight 30671 #checksum 6135
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 145
                                                                                                                                                                                                                                                                                ##molecule_type DNA
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                                                                                                                                                                        Local
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                                                                                                             28 ESQPDPMPDDLHKSSEFTGTMGNMKYLYDDHYVSATKVKSVDKFLAHDLIYNISDKKLKN 87
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                                                    YDKYKTELLNEDLAKKYKDEVVDVYGSNYYVNCYFSSK-DNV-GKVTGG-KTCMYGGITK 144
                                                                                             ESQPDPKPDELHKSSKFTGLMENMKVLYDDNHVSAINVKSIDQFLYFDLIYSIKDTKLGN 60
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HEGNHFDNGNLQNVLVRVYENKRNTISFEVQTDKKSVTAQELDIKARNFLINKKNLYEFN
                               YDNVRVEFKNKDLADKYKDKYVDVFGANYYYQCYFSKKTNDINSHETDKRKTCMYGGVTE 120
                                                                                                                                                      1 Similarity 66.0%;
159; Conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 67.1%;
l Similarity 66.8%;
161; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   *type complete
enterotoxin C3 - Staphylococcus aureus
#formal_name Staphylococcus aureus
19-Mar-1997 #sequence_revision 19-Mar-1997
16-Jul-1999
                                                                                                                                                                                                                                                                                                                  S11885
                                                                                                                                                                                                                                                                                                                                              Mol. Gen. Genet. (1990) 220:329-333
Nucleotide sequence of the staphylococcal enterotoxin gene: sequence comparison of all three Type C staphylococcal enterotoxins.
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#length 266 #molecular-weight 30546 #che
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#superfamily
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28-75,'IL'
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#product enterotoxin C-1 #status experimental #label
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Pred. No. 1.19e-180;
40; Mismatches 34;
                                                                                                                                                                        Score 1156; DB 2;
Pred. No. 7.73e-176;
                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                   Query Match
Best Local :
                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #authors Couch, J.L.; Betley, M.J.
#journal J. Bacteriol. (1989) 171:4507-4510
#title Nucleotide sequence of the type C-3 staphylococcal
enterotoxin gene suggests that intergenic recomb
Causes antigenic variation.
#cross-references_MJID:89327174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #journal Infect. Immun. (1989) 57:2249-2252
#title Conservation of the biologically acti
staphylococcal enterotoxins C1 and
#cross-references_MUID:89277549
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179
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##residues 28-66 ##label BOH2
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##residues 1-266 ##label COU
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NSPYETGYIKFIENE-NSFWYDMMPAPGDKFDQSKYLMMYNDNKMVDSKDVKIEVYLTTK
                                                                                   HEGNHEDNGNLQNVLIRVYENKRNTISFEVQTDKKSVTAQELDIKARNFLINKKNLYEEN 204
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                                                                  HNGNQLDK-Y-RSITVRVFEDGKNLLSFDVQTNKKKVTAQELDYLTRHYLVKNKKLYEFN 178
                                                                                                                                       YDNVRVEFKNKDLADKYKDKYVDVFGANYYYQCYFSKKTNDINSHETDKRKTCMYGGVTE 120
                                                                                                                                                                        YDKVKTELLNEDLAKKYKDEVVDVYGSNYYVNCYFSSK-DNV-GKVTGG-KTCMYGGITK 144
                                                                                                                                                                                                            ESQPDPKPDELHKSSKFTGLMENMKVLYDDNHVSAINVKSIDQFLYFDLIYSIKDTKLGN 60
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                                                                                                                                                                                                                                                                                                   65.1%;
Similarity 65.6%;
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A60114; B60114; A33866
A60114
Bohach, G.A.; Schlievert, P.M.
Bohach, G.A.; Schlievert, P.M.
17-2249-2252
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enterotoxin C-2 precursor - Staphylococcus aureus
enterotoxin C-3 precursor
#formal_name Staphylococcus aureus
10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change
16-Jul-1999
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#product enterotoxin C-2 #status predicted #labe
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                                                                                                                                                                                                                                                                                  40;
                                                                                                                                                                                                                                                                                                   Score 1148; DB 2; Pred. No. 2.05e-174;
                                                                                                                                                                                                                                                                                  Mismatches
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and C2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #ritle Nucleotide sequence of the type A streptococcal exotoxin (erythrogenic toxin) gene from Streptococcus pyogenes bacteriophage T12.
#cross-references MUID:86166804
#accession S29659
                                      #accession
                                                                                                                                                                                                                  #accession
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#accession $18782
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##cross-references EMBL:X61556; NID:947291; PIDN:CAA43754.1; PID:947292
##experimental_source Streptococcus pyogenes strain MGAS165 isolate
Minnesota unassigned phage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##residues 1-251 ##label WEE
##cross-references GB:U40453; EMBL:M19350; NID:g1877426;
PIDN:AAC48868.1; PID:g1877430
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##molecule_type DNA
                                                                                           ##experimental_source Streptococcus pyogenes strain
Arizona unassigned phage
                                                                                                                                                                                                                                                    ##note
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Texas unassigned phage
                                                                                                                                                                                                                                                                                           ##cxperimental_source Streptococcus pyogenes strain MGAS167 !
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##experimental_source Streptococcus pyogenes strain MGAS156 isolate
Nebraska unassigned phage
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J. Exp. Med. (1991) 174:1271-1274
Characterization and clonal distribution of four alleles of
the spea gene encoding pyrogenic exotoxin A (scarlet fever
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        erythrogenic toxin; scarlet fever toxin #formal_name Streptococcus pyogenes phage T 10-Sep-1999 #sequence_revision 10-Sep-1999
                                      S18796
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9659; S18782; S18784; S18785; S18791;
                                                                             the nucleotide sequence was submitted
                                                                                                                                                    9-244 ##label NEY
                                                                                                                                                                                         nucleic acid sequence not shown;
                                                                                                                                                                                                                                    the nucleotide sequence was Library, September 1991
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                  nucleic acid
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                  sequence not
                                                                                                                NID:g47309; PIDN:CAA43753.1; ccus pyogenes strain MGAS327 i
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                    shown;
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                                                                             EMBL Data
                                                                                                                                      PID: 947310
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31-251
                                                                                                                                                                                                                                            #variety
#cross-references
#accession S187
##status
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                                                                                                                                          #authors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 NGNQLDKYRSITVRVFEDGKNLLSFDVQTNKKKVTAQELDYLTRHYLVKNKKLYEFNNSP 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##molecule_type DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YETGYIKFIPKNKESFWFDFFPEP-E-FTQSKYLMIYKDNETLDSNTSQIEVYLTTK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNVRVEFKNKDLADKYKDKYVDVFGANYYYQCYFSKKTNDINSHETDKRKTCMYGGVTEH 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SQPDPKPDELHKSSKFTGLMENMKVLYDDNHVSAINVKSIDQFLYFDLIYSIKDTKLGNY 61
                                                                                                                                                                                                                                                                                                                                                                                                                            YETGYIKFI-ENENSFWYDMMPAPGDKFDQSKYLMMYNDNKMVDSKDVKIEVYLTTK 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h 42.3%;
Similarity 50.2%;
119; Conservative
                                                                                                                                                             S18789
S18782
                    S18789
                                                                                            Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M. J. Exp. Med. (1991) 174:1271-1274
Characterization and clonal distribution of four alleles of
                                                                                                                                                                                                                                                                                    scarlet fever toxin
                                                                                                                                                                                                                                                                                                       S18789 #type fragment
exotoxin A precursor (allele 4) - Streptococcus pyogenes
(strain MGAS262 isolate California) (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #domain signal sequence #status predicted #label 
#product exotoxin type A #status predicted #label 
#length 251 #molecular-weight 29246 #checksum 1475
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#superfamily enterotoxin
                                                                                                                                                                                                                     #formal_name Streptococcus pyogenes
strain MGAS262 isolate California
29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change
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                                                          the speA gene encoding pyrogenic toxin) in Streptococcus pyogenes.
                                                                                                                                                                                                      16-Jul-1999
                                         MUID: 92044323
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nucleic acid sequence
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Pred. No. 1.75e-103;
43; Mismatches 59;
not shown;
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translation not shown
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#authors
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                                                                                                                                                                                                                                                                                                                                                                                                                                     #journal
#title
                                                                                                                                                                                                                                                                                                                                          #title Characterization and clonal distribution of four alleles of the speA gene encoding pyrogenic exotoxin A (scarlet fever toxin) in Streptococcus pyogenes.
#cross-references MUID:92044323
#accession $18783
                                                                                                                                                              #accession
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##residues 1-236 ##label NEA
##cross-references EMBL:X61569; NID:g47313; PIDN:CAA43767.1; PID:g47314
##cross-references EMBL:X61569; NID:g47313; PIDN:CAA43767.1; PID:g47314
##cross-references EMBL:X61569; NID:g47313; PIDN:CAA43767.1; PID:g47314
##cross-references EMBL:Selection of the EMBL Data
##note Library, September 1991
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##cnote the nucleotide sequence was
Library, September 1991
                                                                                                                                                                              ##cross-references EMBL:X61568; NID:947289; PIDN:CAA43766.1; PID:947290 ##experimental_source strain MGAS158 isolate Nebraska unassigned phage the nucleotide sequence was submitted to the EMBL Data Library, September 1991
                                                                                                               ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                        ##status
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                                                                                                                                                                                                                                                                                              ##molecule_type DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YETGYIKFIENEN-SFWYDMMPAPGDKFDQSKYLMMYNDNKMVDSKDVKI 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NGNQLDKYRSITVRVFEDGKNLLSFDVQTNKKKVTAQELDYLTRHYLVKNKKLYEFNNSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DKLKTELKNREMSTLFKNKNVDIYGVEYYYHCYLCR----NA----KRRACIYGGVTNH 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39.98;
1 Similarity 46.58;
107; Conservetion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #formal_name Streptococcus pyogenes phage
strain MGAS188 isolate webraska; strain MGAS485 isolate
Yugoslavia; strain MGAS491 isolate United Kingdom; stra.
MGAS624 isolate Germany; strain MGAS495 isolate Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M. J. Exp. Med. (1991) 174:1271-1274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        $18783 #type fragment exotoxin type A precursor (allele 3) - Streptococcus phage (strain MGAS158 isolate Nebraska and others)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            speA
#superfamily enterotoxin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   scarlet fever toxin
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                                                                                                                                    nucleic acid sequence not shown; translation
                                                                                                                                                                                                                                                                                                                        nucleic acid sequence not shown;
                                                                                                                                                                                                                                                                         1-236 ##label NEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 704; DB 2;
Pred. No. 3.53e-96;
53; Mismatches 54
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                                                                                                                                                                                                                                                                                                                                                                                         189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##experimental_source strain MGAS495 isolate Germany unassigned phage the nucleotide sequence was submitted to the EMBL Data Library, September 1991
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##experimental_source strain MGAS624 isolate Germany unassigned phage
the nucleottide sequence was submitted to the EMBL Data
Library, September 1991
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                                                                                                                                                                                                                                                                                                                                                   182
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Local Similarity 48.3%;
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                                                                                                                                                                                                                                                                                                                                                                                     YETGYIKFIPKNKESFWFDFFPEP-E-FTQSKYLMIYKDNETLDSNTSQI 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGNHLEIPKKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSK 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNVRVEFKNKDLADKYKDKYVDVFGANYYYQCYFSKKTNDINSHETDKRKTCMYGGVTEH 121
S18786;
S18782
                                                                                                            #formal_name Streptococcus pyogenes phage
strain MGAS250 isolate California; strain MGAS251 isolate
California; strain MGAS256 isolate California; strain
MGAS285 isolate Colorado; strain MGAS480 isolate
                                                                                                                                                                                                      s18786 #type fragment
exotoxin type A precursor (allele 2) - Stre
phage (strain MGAS250 isolate California
(fragment)
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#superfamily enterotoxin B
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                                                      MGAS496 isolate Germany
29-Jan-1993 #sequence_revision
                                                                                                                                                                                            scarlet fever toxin
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                                      16-Jul-1999
                                                                                              Yugoslavia; strain MGAS492 isolate United
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the nucleotide sequence was submitted to the EMBL Data Library, September 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #product exotoxin type A (fragment)
#label MAT
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                    S18787; S18788;
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Pred. No. 1.92e-94;
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                  S18790;
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                                                      29-Jan-1993 #text_change
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                    S18792;
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                    S18795; S18799
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CLASSIFICATION KEYWORDS
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##experimental_source strain MGAS251 isolate California unassignd phage
##note the nucleotide sequence was submitted to the EMBL Data
                                                                                                                                                                                                                                                                              ##residues 1-236 ##label NES ##cross-references EMBL:X61567; NID:g47325; PIDN:CAA43765.1; PID:g47326 ##stross-references EMBL:X61567; NID:g47325; PIDN:CAA43765.1; PID:g47326 ##stross-references EMBL MGAS496 isolate Germany unassigned phage ##axperimental_source strain MGAS496 isolate Germany unassigned phage ##mote the nucleotide sequence was submitted to the EMBL Data
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##experimental_source strain MGAS285 isolate Colorado unassigned phage
##note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##cross-references EMBL:X61563; NID:947301; PIDN:CAA43761.1; PID:947302
##experimental_source strain MGAS256 isolate California unassigned phage
##note the nucleotide sequence was submitted to the EMBL Data
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##experimental_source strain MGAS480 isolate Yugoslavia unassigned phage
the nucleotide sequence was submitted to the EMBL Data
##note Library, September 1991
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the speA gene encoding pyrogenic exotoxin A (scarlet fever
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#length
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                       #label SIG\
#product exotoxin type A
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#journal Mol. Gen. Genet. (1986) 203:354-356
#title Streptococcal pyrogenic exotoxin type A (sci
#title is related to Staphylococcus aureus enter
#cross-references_MUID:86284313
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                                                                                                                                                         YIKFI-ENENSFWYDMMPAPGDKFDQSKYLMMYNDNKMVDSKDVKIEVYLTTK 237
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#formal_name Streptococcus sp.
10-Sep-1999 #sequence_revision 10-Sep-1999
             26-Aug-1999
A33953
                                         A33953 #type complete
enterotoxin D precursor - Staphylococcus aureus
#formal_name Staphylococcus aureus
09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change
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Pred. No. 9.49e-94;
44; Mismatches 59;
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#accession A28664
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#journal J. Bacteriol. (1989) 171:4799-4806
#title Genetic and molecular analyses of i
staphylococcal enterotoxin D.
#cross-references MUID:89359112
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##cross-references GB:M18970; NID:g153120; PID:g153121
##experimental_source strain FRI337
[FICATION #superfamily enterotoxin B
ty #length 257 #molecular-weight 2007
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##cross-references GB.W28521; NNID:g1492109; PID:g758691
##CICATION #superfamily enterotoxin B
FICATION #superfamily enterotoxin B
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                                                                    KYRSITVRVFEDGK-NLLSFD-VQTNKKKVTAQELDYLTRHYLVKNKKLYEFN--NSPYE
                                                                                                                                                                                                                                                                              FDSKDIVDKYKGKKVDLYGAYYGYQC----AGG--T--PNK-TACMYGGVTLHDNNRLT 144
                                                                                                                                                                                                                                                                                                                                                   ELHKSSKFTGL-MENMK-VLYDDNHVSAINVKSIDQFLYFDLIYSIKDTKLGNYDNVRVE 67
RGLIVFHTSTEPSVNYDLFGAQGQ-YSNT-LLRIYRDNKTINSENMHIDIYLYT 256
                                                                                                                                     EEKKVPINLWLDGKQNTVPLETVKTNKKNVTVQELDLQARRYLQEKYNLYNSDVFDGKVQ
                                                                                                                                                                                                             FKNKDLADKYKDKYVDVFGANYYYQCYFSKKTNDINSHETDKRKTCMYGGVTEHNGNQLD 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21.3%;
Similarity 35.0%;
82; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Betley, M.J.; Mekalanos, J.J. J. Bacteriol. (1988) 170:34-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #formal_name Staphylococcus aureus 30-Jun-1989 #sequence_revision 30-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A28664 #type complete enterotoxin A precursor -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 375; DB 2;
pred. No. 2.27e-40;
56; Mismatches 77
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Pred. No. 1.85e-46
53; Mismatches 7!
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                                                                                  Query
Best I
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Best Local
                                                                                                                                                                                                                                   #authors Couch, J.L.; Soltis, M.T.; Betley, M.J.
#journal J. Bacteriol. (1988) 170:3954-2960
#title Cloning and nucleotide sequence of the
enterotoxin gene.
#cross-references_MUID:88257005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #authors Huang, I.Y.; Hughes, J.L.; Bergdoll, M.S.; Schantz, E.J.
#journal J. Biol. Chem. (1987) 262:7006-7013
#title Complete amino acid sequence of staphylococcal enterotoxin
#cross-references_MUID:87222293
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                                                                                                                                  ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 TGYIKF-IENENSFWYDMMPAPGDKFDQSKYLMMYNDNKMVDSKDVKIEVYLTT 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##molecule_type protein
##residues 1-233 ##label HUA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
                                                                                  Local
 10
                                 35 DLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTGHPWYNDLLVD 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 DLRKKSELQGTALGNLKQIYYYNEKAKTENKESHDQFLQHTILFKGFFTDHSWYNDLLVD 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
les 82; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                              13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RGLIVFHTSTEPSVNYDLFGAQGQ-YSNT-LLRIYRDNKSINSENMHIDIYLYT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KYRSITVRVFEDGK-NLLSFD-VQTNKKKVTAQELDYLTRHYLVKNKKLYEFN--NSPYE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FDSKDIVDKYKGKKVDLYGAYYGYQC-----AGG--T--PNK-TACMYGGVTLHDNNRLT 120
ELHKSSKFT-GLMENMK-VLYDDNHVSAINVKSIDQFLYFDLIYSIKDTKLGNYDNVRVE 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FKNKDLADKYKDKYVDVFGANYYYQCYFSKKTNDINSHETDKRKTCMYGGVTEHNGNQLD 127
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                                                                    Similarity 79; Conser
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#length
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llarity 35.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                      A28179 #type complete
enterotoxin E precursor - Staphylococcus aureus
#formal_name Staphylococcus aureus
30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change
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05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change
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Pred. No. 4.82e-40;
56; Mismatches 77;
                                                                 Score 329; DB 2; L
Pred. No. 6.51e-33;
56; Mismatches 80;
                                                                                                  Length 257
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#title
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#accession A30509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 IYGGITPAQNNKVN-HKLLGNLFISGESQQNLNNKIILEKDIVTFQEIDFKIRKYLMDNY 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##cross-references GB:M35514; NID:g153820; PID:g153821
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KIYD-ATSPYVSGRIEIGTKDGKHEQIDLFDSPNEG-TRSDIFAKYKDNRIINMKNFSHF 229
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Similarity 25.8%;
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Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.;
Alloni, G.; Azevedo, V.; Bertero, M.G.; Bessieres, P.;
Bolotin, A.; Borchert, S.; Boriss, R.; Boursier, L.; Brans,
A.; Braun, M.; Brignell, S.C.; Bron, S.; Brouillet, S.;
Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
Choi, S.K.; Codani, J.J.; Connerton, I.F.; Cummings, N.J.;
Daniel, R.A.; Denizot, F.; Devine, K.M.; Duesterhoeft, A.;
Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.;
Fabret, C.; Ferrari, E.; Foulger, D.; Fritz, C.; Fujita,
M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galleron, N.; Ghim,
S.Y.; Glaser, P.; Goffeau, A.; Golightly, E.J.; Grandi, G.;
Guiseppi, G.; Guy, B.J.; Haga, K.; Halech, J.; Harwood,
C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.;
Hullo, M.F.; Itaya, M.; Jones, L.; Joris, B.; Karamata, D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       exotoxin
#length 235 #molecular-weight 27560 #checksum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Goshorn, S.C.; Schlievert, P.M.
Infect. Immun. (1988) 56:2518-2520
Nucleotide sequence of streptococci
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exotoxin C precursor - Stre
#formal_name Streptococcus
31-Dec-1988 #sequence_revis
                                                                                                                                                                                                                                                                                                                                 D69832
                                                                                                                                                                                                                                                                                                                                                                    #formal_name Bacillus subtilis
05-Dec-1997 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                  D69832 #type complete
probable Rieske [2Fe-2S] iron-sulfur protein
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Pred. No. 4.19e-08;
37; Mismatches 49; Indels
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#gene
CLASSIFICATION
                                                                                                                                                                                                                                                              Query Match 6.6%;
Best Local Similarity 28.9%;
Matches 24; Conservative
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463,465,481,484
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#title
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##molecule_type DNA
##residues 1-509 ##label KUN
##cross-references GB:Z99109; GB:AL009126; NID:g2633260; PID:e1183041;
##experimental_source strain 168
172 KKLYEFNNSPYETGYIKFIENEN 194
                                                                                                                               116 GGVTE-HNGNQLDKYRSITVRVFEDGKNLLSFDVQTNKKKVTAQ-ELDY--LTRHYLVKN 171
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                                                                                                                                                                 98 ARLY-YEANQNAIDYIKGIVDEH 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Y.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.;
Kurita, K.; Lapidus, A.; Lardinois, S.; Lauber, J.;
Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.;
Maueel, C.; Medigue, C.; Medina, N.; Mellado, R.P.; Mizuno,
M.; Moestl, D.; Nakai, S.; Noback, M.; Noone, D.; O'Reilly,
M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro,
V.; Pohl, T. M.; Portetelle, D.; Porwolik, S.; Prescott,
A.M.; Presecan, E.; Pujic, P.; Purnelle, B.; Rapoport, G.;
Rey, M.; Reynolds, S.; Rieger, M.; Rivolta, C.; Rocha, E.;
Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, E.;
Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchl, J.;
Schowska, A.; Seror, S.J.; Serror, P.; Shin, B.S.; Soldo,
B.; Sorokin, A.; Tacconi, E.; Takagi, T.; Takahashi, H.;
Takemaru, K.; Takeuchi, M.; Tanakoshi, A.; Tanaka, T.;
Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, S.;
Vandenbol, M.; Vannier, F.; Vassarotti, A.; Viari, A.;
Wambutt, R.; Wedler, E.; Wedler, H.; Weitzenegger, T.;
Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto,
K.; Yata, K.; Yoshida, K.; Yoshikawa, H.F.; Zumstein, E.;
Yoshikawa, H.; Danchin, A.
Nature (1997) 390:249-256
The complete genome sequence of the Gram-positive bacterium
Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                             #length 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #superfamily Rieske [2Fe-2S] homology
2Fe-2S; metalloprotein; Rieske iron-sulfur protein
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                                                                                                                                                                                                                                                                                                                                                                                          #domain Rieske [2Fe-2S] homology #label RSK\
#binding_site 2Fe-2S cluster (Cys, His, Cys, His)
(covalent) #status predicted
gth 509 #molecular-weight 57109 #checksum 4843
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                                                                                                                                                                                                                                                              Score 117; DB 2; Le
Pred. No. 5.91e-02;
24; Mismatches 28;
                                                                                                                                                                                                                                                                                                                            Length 509;
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FEATURE

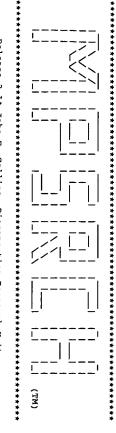
KEYWORDS

SUMMARY

GENETICS

Search completed: Thu Apr 20 15:16:21 2000 Job time: 147 secs.

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Apr 20 15:09:54 2000; MasPar time 26.18 Seconds 632.994 Million cell updates/sec

Tabular output not generated.

Title:

Description:
Perfect Score:
Sequence: >US-09-150-947-12 (1-239) from US09150947.pep 1763 1 ESQPDPKPDELHKSSKFTGL.....NKMVDSKDVKIEVYLTTKKK 239

Scoring table: PAM 150 Gap 11

Searched: 225878 seqs, 69334122 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: sptremb112

1:sp\_archea 2:sp\_bacteria 3:sp\_fungi 4:sp\_human 5:sp\_invertebrate 6:sp\_mammal 7:sp\_mhc 8:sp\_organelle 9:sp\_phage 10:sp\_plant 11:sp\_rodent 12:sp\_unclassified 13:sp\_vertebrate 14:sp\_virus

Statistics: Mean 45.381; Variance 98.387; scale 0.461

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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20 33 44 45 46 47 47 47 47 47 47 47 47 47 47 47 47 47	Result No.
1169 1153 1153 1145 1145 11085 1084 1088 7710 7718 696 694 696 697 698 208	Score
66.3 65.4 64.8 61.5 61.5 61.5 61.5 61.5 61.5 61.5 61.5	Query Match
239 239 2339 2339 2560 2560 2558 2558 2558 2558 2558 2558 2558 255	Length 239
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TOOOO AXXXX	Description ENTEROTOXIN (FRAGMENT)
2. 24e-193 5. 02e-192 2. 73e-189 9. 52e-189 9. 52e-189 2. 31e-177 2. 31e-177 2. 31e-107 3. 06e-107 9. 79e-106 1. 32e-104 4. 20e-103 9. 98e-103 9. 98e-103 1. 03e-102 1. 03e-32 1. 09e-32 1. 141e-21 2. 17e-15	Pred. No.

5	44	43	42	41	0	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21
106	106	106	106	106	108	108	108	109	110	110	110	109	113	112	114	117	117	119	119	130	144	148	148	150
6.0	6.0	6.0	6.0	6.0	6.1	6.1	6.1	6.2	6.2	6.2	6.2	6.2	6.4	6.4	6.5	6.6	6.6	6.7	6.7	7.4	8.2	8.4	8.4	8.5
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YHR214C-BP.	TRANSPOSON TY PUTATIVE	CHROMOSOME XVI READING	CHROMOSOME XII READING	CHROMOSOME VII READING	PEC0195W PROTEIN.	HYPOTHETICAL PROTEIN M	HYPOTHETICAL 26.1 KD P	NAD-SPECIFIC GLUTAMATE	181 (FRAGMENT).	HYPOTHETICAL 47.1 KD P	ORF MSV030 HYPOTHETICA	HYPOTHETICAL 14.5 KD P	CHROMOSOME XIV READING	COMPLETE GENE MAP OF P	FERROUS IRON TRANSPORT	PEPTIDASE, PUTATIVE.	HYPOTHETICAL 57.1 KD P	CARBOXYLESTERASE.	CARBOXYLESTERASE.	SPEX-2 PROTEIN PRECURS	EXTRACELLULAR ENTEROTO	EXOTOXIN H PRECURSOR.	T1M1 ISOLATE SWE88 SPE	ENTEROTOXIN.
5.15e-01	5.15e-01	5.15e-01	5.15e-01	5.15e-01	2.93e-01	2.93e-01	2.93e-01	2.21e-01	1.66e-01	1.66e-01	1.66e-01	2.21e-01	7.02e-02	9.37e-02	5.25e-02	2.18e-02	2.18e-02	1.20e-02	1.20e-02	4.20e-04	4.83e-06	1.30e-06	1.30e-06	6.74e-07

## ALIGNMENTS

Db	о Оу	Оy	Оу	Ma Ma	RESULT OF THE SULT
178 SSPYETGYIKFIENNGNTFWYDMMPAPGDKFDQSKYLMMYNDNKTVDSKSVKIEVHLTTK 237 :                   :	118 HEGNHFDNGKLQNVLIRVYENKRNTISFEVQTDKKSVTAQELDIKARNFLINKKNLYEFN 177  :  :     ::: :  : : :  :  :          : :: :	61 YDKVKTELLNEDLAKKYKDEVVDVYGSNYYVNCYFSSK-DNV-GKVTGG-KTCMYGGITK 117   : :  :              : :           :::	1 ESQPDPTPDELHKASKFTGLMENMKVLYDDRYVSATKVKSVDKFLAHDLIYNISDKKLKN 60 	Query Match 67.6%; Score 1191; DB 2; Length 239; Best Local Similarity 67.6%; Pred. No. 1.27e-197; Matches 163; Conservative 38; Mismatches 34; Indels 6; Gaps 5;	1073678; Q53678; Q1-NOV-1996 (TrEMBLrel. 01, Created) Q1-NOV-1996 (TrEMBLrel. 01, Last sequence update) Q1-NOV-1999 (TrEMBLrel. 12, Last annotation update) Q1-NOV-1999 (TrEMBLrel. 12, Last annotation update) ENTEROTOXIN (FRAGMENT). Staphylococcus aureus. Bactlais firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Staphylococcus. [1] Bacillus/Staphylococcus group; Staphylococcus. [2] SEQUENCE FROM N.A. MEDLINE; 94011313. MARR J.C., LYON J.D., ROBERSON J.R., LUPHER M., BOHACH G.A.; "Characterization of novel type C staphylococcal enterotoxins: biological and evolutionary implications."; Infect Immun. 61:4554-4452(1993). EMBL; L13376; AAA26620.1; HSSP; p34071; ISE2. PROSITE; PS002778; STAPH_STREP_TOXIN_1; 1. PROSITE; PS00278; STAPH_STREP_TOXIN_1; 1. PFAM; PFO1123; Stap_Strp_toxin; 1. Enterotoxin. 1 SEQUENCE 239 AA; 27618 MW; 0810BB9D CRC32;

179

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RESULT
OCCUPANTO
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                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
ENTEROTOXIN TYPE C-7 (SEC740N) (FRAGMENT).
Staphylococcus aureus.
Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MARR J.C., LYON J.D., ROBERSON J.R., LUPHER M., BOHACH G.A.;
"Characterization of novel type C staphylococcal enterotoxins:
blological and evolutionary implications.";
Infect. Immun. 61:4254-4262(1993).
--- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
STAPHYLOCOCCAL FOOD POISONING SYNDROME.
--- SIMILARITY: THE DIFFERENT S. AURRUS ENTEROTOXINS AND S. PYOGENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Last sequence 01-NOV-1999 (TrEMBLrel. 12, Last annotation enterotoxin Type C (SECOVINE) (FRAGMENT).
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01-NOV-1996
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Enterotoxin; Toxin; Superantigen.
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                                                        SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ESQPDPTPDELHKASKFTGLMENMKVLYDDRYVSATKVKSVDKFLAHDLIYNISDKKLKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              K 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          z
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NSPYETGY I KFIENE - NSFWYDMMPAPGDKFDQSKYLMMYNDNKMVDSKDVK I EVYLTTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSPYETGYIKFIENNGNTFWYDMMPAPGDKFDQSKYLMMYNDNKTVDSKSVKIEVHLTTK 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HNGNQLDK-Y-RSITVRVFEDGKNLLSFDVQTNKKKVTAQELDYLTRHYLVKNKKLYEFN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YDNVRVEFKNKDLADKYKDKYVDVFGANYYYQCYFSKKINDINSHETDKRKICMYGGVTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ESQPDPKPDELHKSSKFTGLMENMKVLYDDNHVSAINVKSIDQFLYFDLIYSIKDTKLGN
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161; Conse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              239 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66.3%;
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01, Last sequence update)
12, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         group;
                                                                                                                                group;
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Pred. No. 2.24e-193;
38; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1293E9CA CRC32;
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Query Match
Best Local S
Matches 15
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Best Local S
Matches 15
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Q06531;
                                                                                               NON_TER
SEQUENCE
                                                                                                                                                                                           EMBL;
HSSP;
                                                                                                                                                                                                                                                               MEDLINE; 94011313.

MARR J.C., LYON J.D., ROBERSON J.R., LUPHER M., BOHAC "Characterization of novel type C staphylococcal ente biological and evolutionary implications.";
Infect. Immun. 61:4254-4262(1993).

-I- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE IN STAPHYLOCOCCAL FOOD POISONING SYNDROME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence up
01-NOV-1999 (TrEMBLrel. 12, Last annotation
ENTEROTOXIN TYPE C-4 (SEC4446) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON_TER
SEQUENCE
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EMBL; L13375; AAA26619.1; -.
HSSP; P34071; 1SE2.
PFAM; PF01123; Stap_Strp_toxin: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus aureus.
Bacteria: Firmicutes: Bacillus/Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Characterization of novel type C staphylococcal enterotoxins: biological and evolutionary implications."; Infect. Immun. 61:4254-4262(193).
                                                                                                                                              Enterotoxin; Toxin;
                                                                                                                                                                     PFAM; PF01123; Stap_Strp_toxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-4446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus/Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enterotoxin; Toxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STAPHYLOCOCCAL FOOD POISONING SYNDROME -!- SIMILARITY: THE DIFFERENT S. AUREUS ENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 94011313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MARR J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            238 N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       178 SSPYETGYYKFIENNGNTFWYDMMPAPGDKFDQSKYLMMYNDNKTVDSKSVKIEVHLTTK 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HEGNHFDNGNLQNVLVRVYENKRNTISFEVQTDKKSVTAQELDIKARNFLINKKNLYEFN 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ESQPDPMPDDLHKSSEFTGTMDNMKYLYDDHYYSATKYKSVDKFLAHDLIYNISDKKLKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NSPYETGYIKFIENE-NSFWYDMMPAPGDKFDQSKYLMMYNDNKMVDSKDVKIEVYLTTK 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HNGNQLDK-Y-RSITVRVFEDGKNLLSFDVQTNKKKVTAQELDYLTRHYLVKNKKLYEFN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ESOPDPKPDELHKSSKFTGLMENMKVLYDDNHVSAINVKSIDQFLYFDLIYSIKDTKLGN 60
                                                                                                                                                                                              L13374; AAA26618.1; P34071; 1SE2.
  l Similarity
158; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 238
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159; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   239 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LYON J.D.,
65.4%;
llarity 65.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                               AΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65.9%;
66.0%;
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                                                                                                                                              Superantigen
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                                                                                                 27612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      group;
                                                                                                 WW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WW;
Score 1153; DB 2;
Pred. No. 2.73e-190;
41; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1162; DB 2;
Pred. No. 5.02e-192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                 52B18853 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81CA4BC2 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   update)
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                                             Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                      BOHACH G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
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                                                                                                                                                                                                                                                                                                                                                                                            enterotoxins:
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                                                                                                                                                                                                                                                                       S. PYOGENES
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Q06533;
Q06533;
Q1-NOV-1996 (TrEMBLrel. 01, Created)
Q1-NOV-1996 (TrEMBLrel. 12, Last sequence update)
Q1-NOV-1999 (TrEMBLrel. 12, Last annotation update
ENTEROTOXIN TYPE C (SECCOPELAND) (FRAGMENT).
Staphylococcus aureus.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacteria; Firmicutes; Bacillus/Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-MNCOPELAND;

MEDLINE; 94011313.

MARR J.C., LYON J.D., ROBERSON J.R., LUPHER M., BOHACH G.A.;

"Characterization of novel type C staphylococcal enterotoxins:
biological and evolutionary implications.";

Infect. Immun. 61:4254-4262(1993).

-1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION

STAPHYLOCOCCAL FOOD POISONING SYNDROME.

-1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES

PYROGENIC EXOTOXINS ARE ALL RELATED.

EMBL: L13378; AAA26622.1; -.

EMBL: L13378; AAA26622.1; -.

EMBL: DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES

EMBL: L13378; AAA26622.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                    YDKVKTELLNEDLAKKYKDEVVDVYGSNYYVNCYFSSK-DNV-GKVTGG-KTCMYGGITK 117
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Pred. No. 1.03e-189;
39; Mismatches 37;
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O05157; O75157; O75157;
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Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
STRAIM-95-011195;
EDWARDS V.M., DERINGER J.R., CALLANTINE S.D., DEOBALD C.
BERGER P.H., KAPUR V., STAUFFACHER C.V., BOHACH G.A.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                          Staphylococcus intermedius.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
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                                                                                                                                               SEQUENCE FROM
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PFAM; PF01123;
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DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
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04, Last sequence up
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Pred. No. 9.52e-189;
44; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
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                                                                         C.F.,
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Best Local S
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Q54739; Q54737;
Q54739; Q54737;
Q1-NOV-1996 (TremBLrel. 01:
01-NOV-1996 (TremBLrel. 0:
01-NOV-1999 (TremBLrel. 1:
01-NOV-1999 (TremBLrel. 1:
                                                                                                                                             Streptococcus pyogenes.";
Infect. Immun. 64:1161-1165(1996).
EMBL; U48794; AAB02150.; -.
EMBL; U48792; AAB02148.1; -.
HSSP; P01552; 1SE3.
PFAM; PF01123; Stap_Strp_toxin; 1.
PRINTS; PR00279; BACTRLTOXIN.
SEQUENCE 260 AA; 29767 MW; C8144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE; 94222556.
REDA K.B., KAPUR V., PRICH R.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U91526; AAB50248.1; -.
HSSP; P23313; JUCK.
PROSITE; PS00277; STAPH_STREP_TOXIN_1;
PROSITE: PS00278; STAPH_STREP_TOXIN_2;
PFAM; PF01123; Stap_Strp_toxin; 1.
NON_TER 1 1
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streptococcal superantigen gene (s
Infect. Immun. 62:1867-1874(1994).
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE; 96178602.
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                                                                                                                                                                                                                                                                                                                                "Phylogenetic distribution
variants provides evidence
                                                                                                                                                                                                                                                                                                                                                                       REDA K.B., KAPUR V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus.
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149; Conser
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157; Conser
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llarity 62.6%;
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Pred. No. 2.31e-188;
41; Mismatches 37;
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Last sequence update)
Last annotation update)
                                                                Score 1085; DB 2;
Pred. No. 3.41e-177;
38; Mismatches 44;
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Q54738;
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Infect. Immun. 62:1867-1874(1994).
EMBL; L29565; AAA65928.1; -.
HSSP; P01552; LSE3.
PFAM; PF01123; Stap_Strp_toxin; 1.
PRINTS; PR00279; BACTRLTOXIN.
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Bacteria; Firmicutes; 1
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                                                                                                                     Gremburel.
Gremburel.
Gremburel.
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llarity 62.6%;
Conservative
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      Bacillus/Clostridium
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Last sequence update)
Last annotation updat
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1084; DB 2;
Pred. No. 5.31e-177;
38; Mismatches 44;
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group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus pyogenes.";
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MEDLINE; 94222556.
REDA K.B., KAPUR V.,
RICH R.R.;
                                             Signal.
                                                                                                                                                                                                                                                                                                                               Staphylococcus aureus.
Staphylococcus aureus.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacteria; Firmhylococcus group; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
EXTRACELLULAR ENTEROTOXIN TYPE G PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    085382
085382;
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Infect. Immun. 64:1161-1165(1996).
EMBL; U48793; AAB02149.1; -.
HSSP; P34071; 1SE2.
PFAM; PF01123; Stap_Strp_toxin; 1.
PRINTS; PR00279; BACTRLTOXIN.
                                                                                                            MUNSON S.H., TREMAINE M.T., BETLEY M.J., WELCH R.A.; "Identification and characterization of staphylococcal types G and I from Staphylococcus aureus."; Infect. Immun. 66.3337-3348(1998).
EMBL; AF064773; AAC26660.1; -.
HSSP; P01552; 1SE3.
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MEDLINE; 96178602.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Molecular characterization and phylogenetic distribution of the streptococcal superantigen gene (ssa) from Streptococcus pyogene. Infect. Immun. 62:1867-1874(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REDA K.B., KAPUR V., GOELA D., "Phylogenetic distribution of s variants provides evidence for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
  SEQUENCE
                                                                                             PFAM;
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                                                                                                                                                                                                                                                                               STRAIN-FRI572
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                                                                                           PF01123;
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Similarity 62.4%;
148; Conservative
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                                                                                        Stap_Strp_toxin;
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Pred. No. 2.01e-176;
38; Mismatches 44;
POTENTIAL.
ENTEROTOXIN TYPE
; 14BDEBEE CRC32;
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01-MAY-1999
01-NOV-1999
LT 13
Q54696
Q54696;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9ZNF2
                                                                                                                                                                                                                                                                                         Submitted (JUL-1998) to the EMBL; AB016487; BAA36693.1; HSSP; P01552; 1SE3.
                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus aureus.
Bacteria; Firmicutes; Bacillus/Clostridium
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                                                                                    NNSPYETGYIKFIENEN-SFWYDMMPAPG-DKFDQSKYLMMYNDNKMVDSKDVKIEVYLT
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Similarity 45.6%;
110; Conservative
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llarity 45.2%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                            group; Staphylococcus
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Pred. No. 9.79e-106;
55; Mismatches 65;
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Last sequence update)
Last annotation updat
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54; M
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           PRT;
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1. No. 3.06e-107;
Mismatches 65;
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Best Local
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P97163; P97164;
01-MAY-1997 (TrEMBLrel. 03, Createu,
01-MAY-1997 (TrEMBLrel. 03, Last sequence up,
01-NOV-1999 (TrEMBLrel. 12, Last annotation
OT-NOV-1999 (TREMBLREL 12).
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01-NOV-1996 (TrE)
01-NOV-1999 (TrE)
TYPE A EXOTOXIN I
SPEA.
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J. Exp. Med. 174:1271-1274(1991).

EMBL; X61573; CAA43771.1; -.

EMBL; X61573; CAA43771.1; -.

HSSP; P34071; 1SE2

PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.

PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
   gene encoding pyrogenic exotoxin Streptococcus pyogenes.";
J. Exp. Med. 174:1271-1274(1991).
EMBL; X61556; CAA43754.1; -.
EMBL; X61557; CAA43755.1; -.
EMBL; X61560; CAA43758.1; -.
                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN-MGAS156, AN MEDLINE; 92044323.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P97163
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Bacteria; Firmicutes; F
                                                                                                                                                                              NELSON K., SCHLIEVERT P.M., SELANDER R.K., "Characterization and clonal distribution
                                                                                                                                                                                                                                                                                                                                                            Streptococcus.
                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus pyogenes.
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larity 46.5%;
Conservative
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01, Last sequence up
12, Last annotation
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Pred. No. 1.32e-104;
53; Mismatches 54;
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TYPE A EXOTOXIN.
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r toxin) i
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RESULT
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Best Local S
Matches 11
 Query Match
                                                                                                 gene encoding pyrogenic exotoxin A (scarl Streptcoccus pyogenes.;
J. EXP. Med. 174:1271-1274(1991).
EMBL; X61569; CAA43767.1; -.
EMBL; X61569; CAA43770.1; -.
EMBL; X61572; CAA43770.1; -.
EMBL; X61570; CAA43768.1; -.
EMBL; X61570; CAA43768.1; -.
EMBL; X61571; CAA43769.1; -.
                                                                                                                                                                                                                                                                                                                                  7 15
Q54779 PRELIMINARY; PKI;
Q54779, Q54613; Q54736; Q54740; Q54741;
Q1-NOV-1996 (TIEMBLIFEL 01, Created)
Q1-NOV-1996 (TIEMBLIFEL 11, Last sequence update)
Q1-NOV-1999 (TIEMBLIFEL 12, Last annotation update)
Q1-NOV-1999 (TIEMBLIFEL 12, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X61555; CAA43753.1;
EMBL; X61558; CAA43756.1;
EMBL; X61559; CAA43757.1;
EMBL; X61554; CAA43752.1;
EMBL; X61554; CAA43752.1;
HSSP; P01552; 1SE3.
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                                                                                                                                                                                                                                                        STRAIN=MGAS624 AND MEDLINE; 92044323.
                                                                                                                                                                                                                                                                                                                            Streptococcus pyogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00277; STAPH_STREP_TOXIN_1; PROSITE; PS00278; STAPH_STREP_TOXIN_2; PFAM; PF01123; Stap_Strp_toxin; 1.
                                                                                             PFAM;
                                                                                                                                                                                                                                                                                                                Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                 "Characterization and
                                                                                                                                                                                                                                              NELSON K.,
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      189 YETGYIKFIPKNKESFWFDFFPEP-E-FTQSKYLMIYKDNETLDSNTSQI
|||||||| | :||:| | | :| | ||||:|:|:| |
182 YETGYIKFI-ENENSFWYDMMPAPGDKFDQSKYLMMYNDNKMVDSKDVKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SQPDPKPDELHKSSKFTGLMENMKVLYDDNHVSAINVKSIDQFLYFDLIYSIKDTKLGNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112;
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                       ΑĄ,
                                                                                         Stap_Strp_toxin;
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                       27468
  39.48;
                                                                                                                                                                                                                                              P.M.,
                                                                                                                                                                                                                                 clonal distribution
                                                                                                                                                                                                                                                                                                                Bacillus/Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MW; 81A0C2FE CRC32;
                       WW;
                                                                                                                                                                                                                                                                   AND MGAS485
                                                                                                                                                                                                                                             SELANDER
 Score 694;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 696; DB 2; L
Pred. No. 4.20e-103;
                                             POTENTIAL.
TYPE A EXO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
TYPE A EXOTOXIN.
                      E902ED6D CRC32;
                                              A EXOTOXIN.
                                                                                                                                                                                                                     (scarlet
                                                                                                                                                                                                                                             R.K.,
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f
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of four alleles
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                                                                                                                                                                                                                                                                                                               group;
                                                                                                                                                                                                                                                                                                                                                            update)
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Length 236;
                                                                                                                                                                                                                                                                                                               Streptococcaceae;
                                                                                                                                                                                                                        toxin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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Search completed: Thu Apr 20 15:13:37 2000 Job time: 223 secs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 48.3%; Pred. No. 9.98e-103; Matches 111; Conservative 44; Mismatches 59; Indels 16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                          The stripped of the strip
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